

129

GACCAGCCTG ACCAGCGCCG CCCAACCOCG CCCCAGACAC ATGCTGGGCG GGTACCCCT 2880
 GGGCAACTG ACCAATAGCG GCGGCGGTT CCGCGGGTT ASCAATGCT TCCGATGCC 2940
 GCGCGGGCG TACSTAATGC CCGTGTBCC CGCCGCCCGG TAACGCCAT CCGACGCAA 3000
 TCGGGCCCT CTATCGGGC AGCGATC 3027

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 396 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Val Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
 1 5 10 15
 Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Lys Met Trp
 20 25 30
 Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
 35 40 45
 Val Val Trp Gly Leu Thr Thr Gly Ser Trp Ile Gly Ser Ser Ala Gly
 50 55 60
 Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
 65 70 75 80
 Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
 85 90 95
 Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
 100 105 110
 Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
 115 120 125
 Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met
 130 135 140
 Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Thr Ala Ala
 145 150 155 160
 Thr Ala Thr Glu Ala Leu Leu Pro Phe Glu Asp Ala Pro Leu Ile Thr
 165 170 175
 Asn Pro Gly Gly Leu Leu Glu Gln Ala Val Ala Val Glu Glu Ala Ile
 180 185 190
 Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu

130

195	200	205
Gln Gln Leu Ala Gln Pro Thr Lys Ser Ile Trp Pro Phe Asp Gln Leu 210	215	220
Ser Gln Leu Trp Lys Ala Ile Ser Pro His Leu Ser Pro Leu Ser Asn 225	230	235 240
Ile Val Ser Met Leu Asn Asn His Val Ser Met Thr Asn Ser Gly Val 245	250	255
Ser Met Ala Ser Thr Leu His Ser Met Leu Lys Gly Phe Ala Pro Ala 260	265	270
Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Gln Ala Met 275	280	285
Ser Ser Leu Gly Ser Gln Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu 290	295	300
Gly Ala Gly Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser 305	310	315 320
Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro 325	330	335
Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Gln Thr 340	345	350
Ala Pro Gly His Met Leu Gly Gly Leu Pro Leu Gly Gln Leu Thr Asn 355	360	365
Ser Gly Gly Gly Phe Gly Gly Val Ser Asn Ala Leu Arg Met Pro Pro 370	375	380
Arg Ala Tyr Val Met Pro Arg Val Pro Ala Ala Gly 385	390	395

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1626 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CATCGGAGGG AGTGATCACT ATGCTGTGGG' ACCCAATGCC ACCCGACTAA ATACCGCACC	60
GCTGATGGCC GCGCGGGGTC CGGCTCCAAAT GCTTGCGGGG GCGCGGGGAT GGCAGACGCT	120
TTGGGCGGCT CTGGACGCTC AGGCGCTCGA GTTGACCGCG CGGCTGAACCT CTCTGGCAGA	180
AGGCTGGACT GGAGGTGGCA GCGACAGGCG GCTTGCGGCT GCAACGCGCA TGCTGCTCTG	240

GCTACAAACC GCTCAACAC AGGCCAAGAC CCGTCCGATG CAGCCGACCG CGCAAGCCCG	300
GGCATAACCC CAGGCCATGG CCACGACGCC GTCCGTGCCC GAGTCCGCG CCAACCACT	360
CACCCAGGCC GTCCTTACGG CCACCACTT CTTCCGTATC AACACGATCC CGATCGCGTT	420
GACCGAGATG GATTATTTCA TCCGTATGTG GAACCAAGCA GCCCTGCCAA TCGAGGTCTA	480
CCAGGCGGAG ACCGCGTTA ACACGCTTTT CAGAGAAGTC GAGCCGATGG CGTCGATCCT	540
TGATCCCGGC GCGAGCCAGA GCACGACGAA CCGCATCTTC GGAATGCCCT CCCTTGCCAG	600
CTCAACACCG GTTGGCCTT TCCCGCGGCG GCTACCCAG ACCCTCGGCG AACTGGGTGA	660
GATGAGCGGC CGATGCGAG AGCTGACCCA GCCCTGCGAG CAGGTGACCT CTTTGTTCAG	720
CCAGGTGGGC GGCACCGGCG GCGCAACCC AGCCGACGAG GAAGCCGCGC AGATGGGCTT	780
GCTCGGCACC AGTCCGTGT GGAACCATCC GCTGGCTGGT GATCAGGCC CCAGCGCGGG	840
CGCGGGCTTG CTGCGCGCGG AGTCCCTACC TGGCCGAGGT GGGTCCTTGA CCGGCACGCC	900
GCTGATGTCT CAGTGTATC AAAAGCGGT TGGCCCTCG GTGATGCCCG CGGCTGCTGG	960
CGATCGCTG GCGACGGTG GCGCCCTCC GTTGGGTGG GAGCGATGG GCCAGGGTGC	1020
GCAATCCGCG GGTCCACCA GCGCGGTCT GGTCCGCGCG GCACCGCTCG CCGAGGAGCG	1080
TGAAGAAGAC GACGAGGAG ACTGGGACCA AGAGGACGAC TGTGAGCTC CGTAATGAC	1140
AACGAGCTTC CGGCAACCC GCGCGGAG ACTTGCCAC ATTTTGGCG GGAAGGTAAA	1200
GAGAGAAAT AGTCAGCAT GCGAGAGATC AAGACGATG CGCTACCTT GCGCGAGGAG	1260
GCGGTAAT TCGAGCGAT CTCGCGGAC CTGAAACCC AGATCGACCA GTTGAGTGG	1320
ACGCGAGTT CTTTCAGGG CGATGCGCG GCGCGCGCG GACCGCGCG CCAGCGCGCG	1380
GTGGTGGCT TCCAGAAGC AGCCATAAG CAGAAGCAG AACTGACCA GATCTGAGC	1440
AATATCTTC AGGCGCGCT CCAATCTCG AGGCGCGAG AGGAGCAGCA GCGCGCGTG	1500
TCTTCGAAA TGGGCTTCTG ACCCGCTAT ACGAAAAGAA ACGGAGCAA AACATGACG	1560
AGCAGCACTG GAATTCGCG GGTATCGAG CCGCGCGAG CGCAATCCAG GGAAT	1616

(2) INFORMATION FOR SEQ ID NO:111:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CTAGTGGGATG	GGACCATGGC	CATTTTCTGC	AGTCTCACTG	CCTTCTGTGT	TSACATTTTG	60
GCACGCCGGC	GGAAACGAAG	CACTGGGGTC	GAAGAACGGC	TGGCTTCCCA	TATCGTCCCG	120
AGCTTCGATA	CCTTGGTGG	GGCGGAAGAG	CTTGTCTGTAG	TGGCGCGCCA	TGACAACCTC	180
TCAGAGTGGG	CTCAAACGTA	TAAACACGAG	AAAGGGCGAG	ACCGACGGAA	GGTCAACTTC	240
GGCCGATCCC	GTGTTTGGCT	ATTCTACCGG	AACTGGGGCT	TGCCCTATGC	GAACATCCCA	300
GTGACGTTGC	CTTCGGTCCA	AGCCATTGCC	TGACCGGCTT	CGCTGATGCT	CGCGCCGAGG	360
TTCTGCAGCG	CGTTGTTCAG	CTCGGTAGCC	GTGGCTGCCC	ATTTTTCCTG	GACACCTTGG	420
TACGCTTCCG	AA					432

(2) INFORMATION FOR SPY ID NO. 114.

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

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Met Leu Trp His Ala Met Pro Pro Gln Asn Asn Thr Ala Arg Leu Met
  1      5      10      15
Ala Gly Ala Gly Pro Ala Pro Met Leu Ala Ala Ala Ala Gly Trp Gln
      20      25      30
Thr Leu Ser Ala Ala Leu Asp Ala Gln Ala Val Gln Leu Thr Ala Arg
  35      40      45
Leu Asn Ser Leu Gly Gln Ala Trp Thr Gly Gly Gly Ser Asp Lys Ala
  50      55      60
Leu Ala Ala Ala Thr Pro Met Val Val Trp Leu Gln Thr Ala Ser Thr
  65      70      75      80
Gln Ala Lys Thr Arg Ala Met Gln Ala Thr Ala Gln Ala Ala Ala Tyr
      85      90      95
Thr Gln Ala Met Ala Thr Thr Pro Ser Leu Pro Gln Ile Ala Ala Asn
 100      105      110
His Ile Thr Gln Ala Val Leu Thr Ala Thr Asn Phe Phe Gly Ile Asn
 115      120      125
Thr Ile Pro Ile Ala Leu Thr Gln Met Asp Tyr Phe Ile Arg Met Trp
 130      135      140

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Asn Gln Ala Ala Leu Ala Met Glu Val Tyr Gln Ala Glu Thr Ala Val
 145 150 155 160
 Asn Thr Leu Phe Glu Lys Leu Glu Pro Met Ala Ser Ile Leu Asp Pro
 165 170 175
 Gly Ala Ser Gln Ser Thr Thr Asn Pro Ile Phe Gly Met Pro Ser Pro
 180 185 190
 Gly Ser Ser Thr Pro Val Gly Gln Leu Pro Pro Ala Ala Thr Gln Thr
 195 200 205
 Leu Gly Gln Leu Gly Glu Met Ser Gly Pro Met Gln Gln Leu Thr Gln
 210 215 220
 Pro Leu Gln Gln Val Thr Ser Leu Phe Ser Gln Val Gly Gly Thr Gly
 225 230 235 240
 Gly Gly Asn Pro Ala Asp Glu Glu Ala Ala Gln Met Gly Leu Leu Gly
 245 250 255
 Thr Ser Pro Leu Ser Asn His Pro Leu Ala Gly Gly Ser Gly Pro Ser
 260 265 270
 Ala Gly Ala Gly Leu Leu Arg Ala Glu Ser Leu Pro Gly Ala Gly Gly
 275 280 285
 Ser Leu Thr Arg Thr Pro Leu Met Ser Gln Leu Ile Glu Lys Pro Val
 290 295 300
 Ala Pro Ser Val Met Pro Ala Ala Ala Ala Gly Ser Ser Ala Thr Gly
 305 310 315 320
 Gly Ala Ala Pro Val Gly Ala Gly Ala Met Gly Gln Gly Ala Gln Ser
 325 330 335
 Gly Gly Ser Thr Arg Pro Gly Leu Val Ala Pro Ala Pro Leu Ala Gln
 340 345 350
 Glu Arg Glu Glu Asp Asp Glu Asp Asp Trp Asp Glu Glu Asp Asp Trp
 355 360 365

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Met Ala Glu Met Lys Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly
 1 5 10 15

1000

Asn Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Glu Ile Asp Glu Val
 20 35 30
 Glu Ser Thr Ala Gly Ser Leu Glu Gly Glu Trp Arg Gly Ala Ala Gly
 15 40 45
 Thr Ala Ala Glu Ala Ala Val Val Arg Phe Glu Glu Ala Ala Asn Lys
 50 55 60
 Glu Lys Glu Glu Leu Asp Glu Ile Ser Thr Asn Ile Arg Glu Ala Gly
 65 70 75 80
 Val Glu Tyr Ser Arg Ala Asp Glu Glu Glu Glu Glu Ala Leu Ser Ser
 85 90 95
 Glu Met Gly Phe
 100

(2) INFORMATION FOR SEQ ID NO. 126:

(4) SEQUENCE CHARACTERISTICS.

- (A) LENGTH: 366 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO: 116.

GATCTCCGGC	GACTTGAAAA	CCGAGATCGA	CCAGGTGGAG	TCGACGGCAG	GTTCCTTGCA	60
GGGCCAGTGG	CGGGGGGCGG	GGGGGACGGC	CGCCCAAGCC	GGGTGTGTTC	GCCTTCCAGA	120
AGCAGCCCAAT	AAGCAGAGGC	AGGAAGTCCA	CGAGATCTCG	ACGAATATTC	GTCAAGGCGCG	180
CTTCCATATC	TGGAGGGGCG	ACGAGGAGCA	GCAGCAGGCG	CTGTCTCTCC	AAATGGGCTT	240
CTGACCCGCT	AATACGAAAA	GAAACCGAGC	AAAAACATGA	CAGAGCAGCA	GTGGAATTTT	300
GGGGTATCG	AGGCGGCGGC	AAGCGCAATC	CAGGGAAATG	TCAGTCCAT	TCATTCCTTC	360
CTTGACGAGG	GGAAGCAGTC	CCTGACCAAG	CTGGCA			396

(2) INFORMATION FOR SEQ ID NO:117:

(1) SEQUENCE CHARACTERISTICS.

- (A) LENGTH: 80 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:117.

11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 10

135

Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln
 20 25 30
 Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu
 35 40 45
 Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser
 50 55 60
 Arg Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
 65 70 75 80

(2) INFORMATION FOR SEQ ID NO:118:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 387 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GTGGATCCCG ATCCCGTGTG TCGCTATTCT ACCCGAAGTC GCGGTTGCCC TATGCGAACA 60
 TCCCAATGAC GTTGCTTTCT GTCGAAGCCA TTGCTTGACC GCGTTGCTG ATGCTCCGCG 120
 CCAGTTTCTG CAGCGCCTTG TTCACTCGG TAGCCGTGGC GTCCCATTTT TCGTGGACAC 180
 CCGGTAGCG CTCGAACCG CTACGCCCC AGCGCGCTGC GAGCTTGCTC AGGACTGCT 240
 TCCCTCTCTC AAGGAGGGAA TGAATGGAGC TGACATTTTC CTGGATTGCG CTTGCGCGCG 300
 CCTCGATACC CGCAAAATTC CAGTCTGCT CTGTATGTT TTGCTCTGCT TCTTTTCTCT 360
 ATTAGCGGCT CAGAAGCCCA TTGCGA 387

(2) INFORMATION FOR SEQ ID NO:119:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 272 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CGGCAGGAGG ATCTCGTTG GCGCAACGCG CTTGGCGAGG GCTCCGTTCC GGGGCGGAGC 60
 TCGCGCGCGG ATGCTTCTCT TGCCCGCAGC CGCGCCTGGA TCGATGGACC AGTTCCTACC 120
 TTCCCGACCT TTCTTCGCT GTCTGTGCGA TAGCGGTGAC CCGCGCGCGC ACCTCGGAG 180
 TTTTGGCGCG CAGCGCGGCT CCGTGGTTG GCGCGGAGC CAGACGCTT GCACCGAACC 240

GGGCGGGGGTT GCGCGATTGG CATCTTTGGC CA

272

(2) INFORMATION FOR SEQ ID NO:120:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Asp	Pro	Val	Asp	Ala	Val	Ile	Asn	Thr	Thr	Cys	Asn	Tyr	Gly	Gln	Val
1				5					10					15	
Val Ala Ala Leu															
20															

(2) INFORMATION FOR SEQ ID NO:121:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Ala	Val	Glu	Ser	Gly	Met	Leu	Ala	Leu	Gly	Thr	Pro	Ala	Pro	Ser
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:122:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Ala	Ala	Met	Lys	Pro	Arg	Thr	Gly	Asp	Gly	Pro	Leu	Glu	Ala	Ala	Lys
1				5					10					15	
Glu Gly Arg															

(2) INFORMATION FOR SEQ ID NO:123:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp Pro Ala Trp Gly Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Asp Ile Gly Ser Glu Ser Thr Glu Asp Gln Gln Xaa Ala Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Ala Glu Glu Ser Ile Ser Thr Xaa Glu Xaa Ile Val Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Asp Pro Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro
1 5 10 15

Ser

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Ala	Pro	Lys	Thr	Tyr	Xaa	Glu	Glu	Leu	Lys	Gly	Thr	Asp	Thr	Gly
1					5				10					15

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Asp	Pro	Ala	Ser	Ala	Pro	Asp	Val	Pro	Thr	Ala	Ala	Gln	Leu	Thr	Ser
1				5				10							15
Leu	Leu	Asn	Ser	Leu	Ala	Asp	Pro	Asn	Val	Ser	Phe	Ala	Asn		
		20					25						30		

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Asp	Pro	Pro	Asp	Pro	His	Gln	Xaa	Asp	Met	Thr	Lys	Gly	Tyr	Tyr	Pro
1				5				10							15
Gly	Gly	Arg	Arg	Xaa	Phe										
				20											

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asp	Pro	Gly	Tyr	Thr	Pro	Gly
1				5		

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: /note= "The Second Residue Can Be Either a Pro or Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Xaa Xaa Gly Phe Thr Gly Pro Gln Phe Tyr
 1 5 10

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: /note= "The Third Residue Can Be Either a Gln or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Xaa Pro Xaa Val Thr Ala Tyr Ala Gly
 1 5

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Xaa Xaa Xaa Glu Lys Pro Phe Leu Arg
 1 5

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Xaa Asp Ser Glu Lys Ser Ala Thr Ile Lys Val Thr Asp Ala Ser
 1 5 10 13

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Ala	Gly	Asp	Thr	Xaa	Ile	Tyr	Ile	Val	Gly	Asn	Leu	Thr	Ala	Asp
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Ala	Pro	Glu	Ser	Gly	Ala	Gly	Leu	Gly	Gly	Thr	Val	Gln	Ala	Gly
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Xaa	Tyr	Ile	Ala	Tyr	Xaa	Thr	Thr	Ala	Gly	Ile	Val	Pro	Gly	Lys	Ile
1				5					10					15	
Asn	Val	His	Leu	Val											
			20												

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 862 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

141

GCAACGCTGT	CGTGGCTTT	GCGGTGATCG	GTTTCGCTTC	GCTGCGGGTG	GCGGTGGCGG	60
TCACCATCCG	ACCGACCGCG	GCTCAAAAC	CGGTAGAGGG	ACACCAAAC	GCCCAGCCAG	120
GGAAGTTTAT	GCGTTGTTG	CCGACGCAAC	AGCAGGCGCC	GCTCCGCGCG	CCTCCGCCCG	180
ATGATCCAC	CGCTGGATTC	CAGGCGCGCA	CCATTCCGGC	TGTACAGAAC	GTGGTCCCGC	240
GGCGGGGTAC	CTCACC CGCG	GTGGGTGGGA	CGCGGGCTTC	GCTTGGCGCG	GAAGCGCCCG	300
CGTGGCGCGG	TGTTGTGCTT	GCTCCGGTGC	CAATCCCGGT	CCCGATCCTC	ATTCCCCCGT	360
TCCGGGGTTG	GCAGCCTGGA	ATGCCGACCA	TCCCAACCGC	ACCGCGGACG	ACGCGGGTGA	420
CCACGTGGGC	GACGACCGCG	CGGACCAAGC	CGCCGACCAC	GCCGGTGACC	ACGCCGCTAA	480
CGACGCGCGC	GACCAACCGG	GTGACCACGC	CGCAACGAC	GCGCGCGACC	ACGCCGCTGA	540
CCACGCCACC	AACGACTGTC	GCTCCGACGA	CGTCCGCCCC	GACGACGCTC	GCTCCGACCA	600
CGTCCGCCCC	GACCAACGTC	GCTCCGACGA	CGCCACCGCC	GACGACGCTC	GCTCCGACGC	660
CGACGCAGCA	GCCCCGCAAA	CAACCAACCC	AACAGATGCC	AACCCAGCAG	CGGACCGTGG	720
CCCCGCAGAC	GCTGGCGCGG	GCTCCGACGC	CGCCGTCCCG	TGCTCCCAAC	GGCAGCGCGG	780
GGGGCGACTT	ATTCCGCGCG	TTCTGATCAC	GCTCCGCGCT	TCACTACGCT	CGGAGGACAT	840
GGCGGGTGAT	GCGGTGACCG	TGGTGCTGCC	CTGTCTCAAC	GA		882

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

CCATCAACCA	ACCGGTGCGG	CGCGCGCGCG	CGCGGATCC	GCGGTGCGCG	CCACGCGCGC	60
CGGTGCTTCC	GCTGCGCGCG	TGCGCGCGCT	CGCGCGCTTC	GCGCGCGACC	GGGTGGGTGC	120
CTAGGGCGCT	GTTACCGCGC	TGGTGGCGCG	GGACGCGCGC	GGCACCACCG	GTACCGCGCA	180
TGGCGCGCTT	GCGCGCGCGG	GCACCGTTGC	CACCGTTGCC	ACCGTTGCCA	CGGTGGCGGA	240
CCAGCCACCC	GCGCGGACCA	CGCGCACCGC	CGCGCGCGCG	CGCACCGCTG	GGGTGGCGCT	300
TGGTGGCGCT	ACCGCGCGCA	CGCGCGTTGC	CGCGGTCAAC	GCGGACGGA	CTACCGCGCG	360
ACCGCGCGCT	CGCGCGCGCG	CGCGCGCGAC	CGCGATTGCC	ACCGCGCTCA	CGCGCGCGCT	420

142

```

GGAGTGCCEC GATTAGGGCA CTGACCGGCG CAACCAAGCC AAGTACTCTC GGTCAACCGAG      480
CACTTCCAGA CGACACCACA GCACGGGGTT GTCCGCCGAC TGGGTGAAAT GGCAGCCGAT      540
AGCGGCTAGC TGTCGGCTGC GTTCACCTC GATCATGATG TCSAGGTEAC CGTGACCGCG      600
CCCCCGAAG GAGGCGCTGA ACTCGGCGTT GAGCGGATCG GCGATCGGTT GGGGCAGTGC      660
CCAGGCCAAT ACGGGGATAC CCGGTGTCTA AGCGGCCGCG AGCGCAGCTT CGGTTGCGCG      720
ACNCTGCTCG GGGTGGCCTG TTACGCGCTT GTCTTCGAAC ACGAGTAGCA GGTCTGCTCC      780
GGCGAGGCA TCCACCACGC GTTCGCTCAG CTEST
                                                                815

```

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```

ACCAGCCGCC GGCTGAGGTC TCAGATCAGA GATCTCCCGG ACTCACCAGG GCGGTTCCAGC      60
CTTCTCCAG AACAACTGCT GAAGATCCTC GCGCGCGAAA CAGGCGCTGA TTGAACGCTC      120
TATGACCGGT TGAACGACGA GATCATCCCG CAGATTGATA TGACACCGCT GGCTTACAG      180
GTGCGCAAGA TGCTGCAGCT GTATGTCTCG GACTCCGTGT CCGGATCAG CTTTGCCGAC      240
GGCCGGGTGA TCGTGTGAG CGAGGAGCTC GGCAGAGGCC AGTATCCGAT CGAGACGCTG      300
GACCGCATCA CGCTGTTTGG GCGGCCGACG ATGACAACGC CCTTCATGCT TGAGATGCTC      360
AAGCGTGAAC GCGACATCCA GCTCTTCAGG ACCGACGGCC ACTACCAGGG CCGGATCTCA      420
ACACCCGACG TGTCTACGC GCGCGGCTC CGTCAGCAAG TTCACCGCAC CGACGATCCT      480
GCGTTCTGCC TGTCGTTAAG CAAGCGGATC GTCTCGAGCA AGATCCTGAA TCAGCAGGCC      540
TTGATTGCGG CACACAGTC GGGGAAGAC GTTCTGAGA GCATCCGAC GATGAAGCAC      600
TCGCTGCTCT GGTTCGATCG ATCGGGCTCC GTGGCGGAGT TGAACGGGTT CGAGCGAAT      660
GCGGCAAGG CATACTTCAC CCGCTGGGG CATCTCTCTC CCGAGGAGTT CGCATTCGAG      720
GGCGGCTCGA CTGGCGCGCC GTTGACGCC TTCAACTCGA TGGTCAGCTT CGGCTATTCT      780
CTGCTGTACA AGAACATCAT AGGGCGGATC GAGGCTGACA GCGTGAACGC GTATATCGGT      840

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143

```

TTCCTACACC AGGATTCACG AGGGCACGCA ACGTCTCGTG CCGAATTCGG CACGAGCTCC      900
GCTGAAACCG CTGSCCGGCT GCTCAGTGGC CTTACGTAAT CCGCTGCGCC CAGGCGCGCC      960
CCCCGGCCGA ATACCAGCAG ATCGGACAGC GAATTGCGGC CCAGCGGTTT GGAGCCCTGC      1020
ATACCGCCCG CACACTCACC GGCAGCGAAC AGGCTTGCCA CCGTGGCGGC GCCGCTGTTC      1080
GCGTCTACTT CGACACCGCC CATCACGTAG TGACACGTGG GCGCGACTTC CATTCCTTGC      1140
GTTCGGCAGG AG
                                                                1152

```

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 655 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

```

CTCGTGCCGA TTCGGCAGGG TGTACTTGCC GGTGGTGTAN GCGGCATGAG TGCCGACGAC      60
CAGCAATGCG GCAACAGCAC GGATCCCCGT CAACGACGCC ACCCGGTCCA COTGGGCGAT      120
CCGCTCGAGT CCGCCCTGGG CGGCTCTTTC CTGCGGCAGG GTCATCGAC GTGTTTCTGC      180
CSTGGTTTGC CGCCATTATG CCGCGCGGCG GCGTCGGGCG GCCGATATGG CCGAANGTGG      240
ATCAGCACAC CCGAGATACG GGTCTGTGCA AGCTTTTTGA GCGTCGCGCG GGGCAGCTTC      300
GCCGSCAATT CTACTAGCGA GAAGTCTGGC CCGATACGGA TCTGACCGAA GTGCTGCGG      360
TGCAGCCAC CTTCAATTGC GATGGCGGCG ACGATGGCGC CTGACCGGAT CTTGTSCCGC      420
TTGCCGACGG CGACGCGGTA GGTGGTCAAG TCCGCTCTAC GCTTGGGCTT TTGCGGACGG      480
TCCCGACGCT GGTGCGGTTT GCGCGCGGAA AGCGGCGGGT CCGGTGCCAT CAGGAATGCC      540
TCACCGCCGC GSCACTGCAC GGCAGTGCC GCGCGGATGT CAGCCATCGG GACATCATGC      600
TCGCGTTTAT ACTCTCGAC CAGTCGCGCG AACAGCTCGA TTCCCGGACC GCCCA      655

```

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

```

Asn Ala Val Val Ala Phe Ala Val Ile Gly Phe Ala Ser Leu Ala Val
1           5           10           15

Ala Val Ala Val Thr Ile Arg Pro Thr Ala Ala Ser Lys Pro Val Gln
20           25           30

Gly His Gln Asn Ala Gln Pro Gly Lys Phe Met Pro Leu Leu Pro Thr
35           40           45

Gln Gln Gln Ala Pro Val Pro Pro Pro Pro Pro Asp Asp Pro Thr Ala
50           55           60

Gly Phe Gln Gly Gly Thr Ile Pro Ala Val Gln Asn Val Val Pro Arg
65           70           75           80

Pro Gly Thr Ser Pro Gly Val Gly Gly Thr Pro Ala Ser Pro Ala Pro
85           90           95

Gln Ala Pro Ala Val Pro Gly Val Val Pro Ala Pro Val Pro Ile Pro
100          105          110

Val Pro Ile Ile Ile Pro Pro Phe Pro Gly Trp Gln Pro Gly Met Pro
115          120          125

Thr Ile Pro Thr Ala Pro Pro Thr Thr Pro Val Thr Thr Ser Ala Thr
130          135          140

Thr Pro Pro Thr Thr Pro Pro Thr Thr Pro Val Thr Thr Pro Pro Thr
145          150          155          160

Thr Pro Pro Thr Thr Pro Val Thr Thr Pro Pro Thr Thr Pro Pro Thr
165          170          175

Thr Pro Val Thr Thr Pro Pro Thr Thr Val Ala Pro Thr Thr Val Ala
180          185          190

Pro Thr Thr Val Ala Pro Thr Thr Val Ala Pro Thr Thr Val Ala Pro
195          200          205

Ala Thr Ala Thr Pro Thr Thr Val Ala Pro Gln Pro Thr Gln Gln Pro
210          215          220

Thr Gln Gln Pro Thr Gln Gln Met Pro Thr Gln Gln Gln Thr Val Ala
225          230          235          240

Pro Gln Thr Val Ala Pro Ala Pro Gln Pro Pro Ser Gly Gly Arg Asn
245          250          255

Gly Ser Gly Gly Gly Asp Leu Phe Gly Gly Phe
260          265

```

(3) INFORMATION FOR SEQ ID NO:143:

145

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

```

Ile Asn Gln Pro Leu Ala Pro Pro Ala Pro Pro Asp Pro Pro Ser Pro
1           5           10           15

Pro Arg Pro Pro Val Pro Pro Val Pro Pro Leu Pro Pro Ser Pro Pro
          20           25           30

Ser Pro Pro Thr Gly Trp Val Pro Arg Ala Leu Leu Pro Pro Trp Leu
          35           40           45

Ala Gly Thr Pro Pro Ala Pro Pro Val Pro Pro Met Ala Pro Leu Pro
          50           55           60

Pro Ala Ala Pro Leu Pro Pro Leu Pro Pro Leu Pro Pro Leu Pro Thr
          65           70           75           80

Ser His Pro Pro Arg Pro Pro Ala Pro Pro Ala Pro Pro Ala Pro Pro
          85           90           95

Ala Cys Pro Phe Val Pro Val Pro Pro Ala Pro Pro Leu Pro Pro Ser
          100          105          110

Pro Pro Thr Glu Leu Pro Ala Asp Ala Ala Cys Pro Pro Ala Pro Pro
          115          120          125

Ala Pro Pro Leu Ala Pro Pro Ser Pro Pro Ala Gly Ser Ala Ala Ile
          130          135          140

Arg Ala Leu Thr Gly Ala Thr Ser Ala Ser Thr Leu Gly His Arg Ala
          145          150          155          160

Leu Pro Asp Asp Thr Thr Ala Arg Gly Cys Arg Arg Thr Gly
          165          170

```

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

146

Gln Pro Pro Ala Glu Val Ser Asp Gln Arg Val Ser Gly Leu Thr Gly
 1 5 10 15
 Ala Val Gln Pro Ser Pro Arg Thr Thr Ala Glu Asp Pro Arg Pro Arg
 20 25 30
 Asn Arg Arg
 35

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Arg Ala Asp Ser Ala Gly Cys Thr Cys Arg Trp Cys Xaa Pro His Glu
 1 5 10 15
 Cys Arg Arg Pro Ala Met Arg Gln Gln His Gly Ser Arg Ser Thr Thr
 20 25 30
 Pro Pro Gly Pro Arg Gly Arg Ser Ala Arg Val Arg Pro Gly Arg Leu
 35 40 45
 Phe Pro Trp Ala Gly Ser Ser Asp Val Phe Pro Pro Trp Phe Ala Ala
 50 55 60
 Ile Met Pro Ala Arg Arg Val Gly Arg Pro Val Trp Pro Xaa Val Asp
 65 70 75 80
 Gln His Thr Arg Asp Thr Gly Leu Cys Lys Leu Phe Glu Arg Arg Ala
 85 90 95
 Gly Gln Leu Arg Arg Gln Phe Tyr
 100

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

147

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GGATCCATAT GGGCCATCAT CATCATCATC ACGTGATCGA CATCATGGGG ACC

53

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR Primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CCTGAATTCA GGCCTCGGTT GCGCCGCGCT CATCTTGAAC GA

42

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR Primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GGATCCTGCA GGCTCGAAAC CACCGAGCGG T

31

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CTCTGAATTC AGCGCTGGAA ATCGTCCGCA T

31

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GGATCCAGCC CTGAGATGAA GACCGATGCC GCT

33

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GAGAGAAATTC TCAGAAGCCC ATTTGCCAGG ACA

33

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 182..1373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

TGTTCTTCCG	CGGCAGGCTG	GTGGAGGAAG	GGGCCACCGA	ACAGCTGTTT	TCCTCGCCGA	60
AGCATGCGGA	AACCCGCCGA	TACCTCGCCG	GACTGTGCGG	GGAGCTCAAG	GACGCCAAGC	120
GCAGAAATTG	AAGAGCACAG	AAAGGTATGG	C GTG AAA ATT CGT TTG CTT ACG			172
			Val Lys Ile Arg Leu His Thr			
			1		5	
CTG TTG GCC GTG TTG ACC GCT GCG CCG CTG CTG CTA GCA GCG GCG GCG						220
Leu Leu Ala Val Leu Thr Ala Ala Pro Leu Leu Leu Ala Ala Ala Gly						
	10		15		20	
TGT GGC TCG AAA CCA CCG AGC GGT TCG CCT GAA ACG GGC GCC GGC GGC						268
Cys Gly Ser Lys Pro Pro Ser Gly Ser Pro Glu Thr Gly Ala Gly Ala						
	25		30		35	
GGT ACT GTC GCG ACT ACC CCC GCG TCG TCG CCG CTG ACG TTG GCG GAG						316
Gly Thr Val Ala Thr Thr Pro Ala Ser Ser Pro Val Thr Leu Ala Glu						
	40		45		50	55
ACC GGT AGC ACG CTG CTC TAC CCG CTG TTC AAC CTG TGG GGT CCG GCC						364
Thr Gly Ser Thr Leu Leu Tyr Pro Leu Phe Asn Leu Trp Gly Pro Ala						
		60		65		70
TTC CAC GAG ACG TAT CCG AAC GTC ACG ATC ACC GCT CAG GGC ACC GGT						412
Phe His Glu Arg Tyr Pro Asn Val Thr Ile Thr Ala Gln Gly Thr Gly						
		75		80		85
TCT GGT GCC GCG ATC GCG CAG GCC GCC GGC GCG ACG GTC AAC ATT GCG						460
Ser Gly Ala Gly Ile Ala Gln Ala Ala Ala Gly Thr Val Asn Ile Gly						
	90		95		100	
GCC TCC GAC GCC TAT CTG TCG GAA GGT GAT ATG GGC GCG CAC AAG GCG						508
Ala Ser Asp Ala Tyr Leu Ser Glu Gly Asp Met Ala Ala His Lys Gly						
	105		110		115	
CTG ATG AAC ATC GCG CTA GCC ATC TCC GGT CAG CAG GTC AAC TAC AAC						556
Leu Met Asn Ile Ala Leu Ala Ile Ser Ala Gln Gln Val Asn Tyr Asn						
	120		125		130	135
CTG CCC GGA GTG AGC GAG CAC CTC AAG CTG AAC GGA AAA GTC CTG GCG						604
Leu Pro Gly Val Ser Glu His Leu Lys Leu Asn Gly Lys Val Leu Ala						
		140		145		150
GCC ATG TAC CAG GGC ACC ATC AAA ACC TGG GAC GAC CCG CAG ATC GCT						652
Ala Met Tyr Gln Gly Thr Ile Lys Thr Trp Asp Asp Pro Gln Ile Ala						
	155		160		165	
GCG CTC AAC CCC GCG GTG AAC CTG CCC GGC ACC GCG GTA GTT CCG CTG						700
Ala Leu Asn Pro Gly Val Asn Leu Pro Gly Thr Ala Val Val Pro Leu						

150

170	175	180	
CAC CCG TCC GAC GGG TCC GGT GAC ACC TTC TTG TTC ACC CAG TAC CTG			740
His Arg Ser Asp Gly Ser Gly Asp Thr Phe Leu Phe Thr Gln Tyr Leu			
185	190	195	
TCC AAG CAA GAT CCC GAG GGC TCG GGC AAG TCG CCC GGC TTC GGC ACC			795
Ser Lys Gln Asp Pro Glu Gly Trp Gly Lys Ser Pro Gly Phe Gly Thr			
200	205	210	215
ACC GTC GAC TTC CCG GCG GTG CCG GGT GCG CTG GGT GAG AAC GGC AAC			844
Thr Val Asp Phe Pro Ala Val Pro Gly Ala Leu Gly Glu Asn Gly Asn			
220	225	230	
GCC GGC ATG GTG ACC GGT TGC GCC GAG ACA CCG GGC TGC GTG GCC TAT			892
Gly Gly Met Val Thr Gly Cys Ala Glu Thr Pro Gly Cys Val Ala Tyr			
235	240	245	
ATC GGC ATC ACC TTC CTC GAC CAG GCG AGT CAA CCG GGA CTC GGC GAG			940
Ile Gly Ile Ser Phe Leu Asp Gln Ala Ser Gln Arg Gly Leu Gly Glu			
250	255	260	
GCC CAA CTA GGC AAT AGC TCT GCC AAT TTC TTG TTG CCC GAC GCG CAA			988
Ala Gln Leu Gly Asn Ser Ser Gly Asn Phe Leu Leu Pro Asp Ala Gln			
265	270	275	
AGC ATT CAG GCC GCG GCG GCT GGC TTC GCA TCG AAA ACC CCG GCG AAC			1036
Ser Ile Gln Ala Ala Ala Ala Gly Phe Ala Ser Lys Thr Pro Ala Asn			
280	285	290	295
CAG GCG ATT TCG ATG ATC GAC GCG CCC GGC CCG GAC GGC TAC CCG ATC			1084
Gln Ala Ile Ser Met Ile Asp Gly Pro Ala Pro Asp Gly Tyr Pro Ile			
300	305	310	
ATC AAC TAC GAG TAC GCC ATC GTC AAC AAC CCG CAA AAG GAC GCC GCC			1132
Ile Asn Tyr Glu Tyr Ala Ile Val Asn Asn Arg Gln Lys Asp Ala Ala			
315	320	325	
ACC GCG CAG ACC TTG CAG GCA TTT CTG CAC TCG GCG ATC ACC GAC GGC			1180
Thr Ala Gln Thr Leu Gln Ala Phe Leu His Trp Ala Ile Thr Asp Gly			
330	335	340	
AAC AAG GCC TCG TTC CTC GAC CAG GTT CAT TTC CAG CCG CTG CCG CCC			1228
Asn Lys Ala Ser Phe Leu Asp Gln Val His Phe Gln Pro Leu Pro Pro			
345	350	355	
GCG GTG GTG AAG TTG TCT GAC GCG TTG ATC GCG ACG ATT TCC AGC			1272
Ala Val Val Lys Leu Ser Asp Ala Leu Ile Ala Thr Ile Ser Ser			
360	365	370	
TAGCCTCGTT GACCACCAG CGACAGCAAC CTCGTCGGG CCATCGGGCT GCTTTGCGGA			1320
GCATGCTGGC CCGTGCCGGT GAAGTGGGCC GCGTGGGCC GGCATCCGG TCGTTGGGTG			1368
GGATAGGTGC GGTGATCCCG CTGCTTGGCC TGCTCTTGGT GCTGTTGGTG CTGGTATCC			1416

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AGGCGATGGG TCCGATCAGG CTCACCGGGT TGCATTTCTT CACCGCCACC GAATGGAATC 1513
CAGGCAACAC CTACGCGCAA ACGTTGTCA CCGACCGCTC GCCCATCCCG TCGGCGCTTA 1573
CTACGGGGGG TTGCGGCTGA TCTCGGGAC GCTGGCGACC TCGGCAATCG CCTGATCAT 1633
CGCGGTGCGG GTCTCTGTAG GAGCGGCGCT GTTGATCGTG GAACGGCTGC CGAAACGGTT 1693
GGCCGAGGCT GTGGGAATAG TCTGGAATT GCTGCGCGGA ATCCCCAGCG TGGTCGTCGG 1753
TTTGTGGGGG GCAATGACCT TCGGGCCGTT CATCGCTCAT CACATCGCTC CGGTGATCCG 1813
TCACAACGCT CCGGATGTGC CGGTGCTGAA CTACTTGGCG GCGGACCCCG GCAACGGGGA 1873
GGGCGTGTG GTGTCCCGTC TGGTGTGGC GGTGATGCTC GTTCCCATTA TCGCCACCAC 1933
CACTCATGAC CTGTTCGGGC AGGTGCGGCT GTTCCCCCGG GAGGCGCCGA TCGGGAATTC 1993

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(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

```

Val Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro
 1             5             10             15
Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
 20             25             30
Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
 35             40             45
Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
 50             55             60
Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
 65             70             75             80
Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
 85             90             95
Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
100             105             110
Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
115             120             125
Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys

```

152

130	135	140
Leu Asn Gly Lys Val	Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr	
145	150	155 160
Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro		
	165	170 175
Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr		
	180	185 190
Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Gln Gly Trp Gly		
	195	200 205
Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly		
	210	215 220
Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu		
	225	230 235 240
Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala		
	245	250 255
Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn		
	260	265 270
Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala Gly Phe		
	275	280 285
Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro		
	290	295 300
Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn		
	305	310 315 320
Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu		
	325	330 335
His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val		
	340	345 350
His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu		
	355	360 365
Ile Ala Thr Ile Ser Ser		
	370	

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:154:

TGTTCTTCGA	CGGCAGGCTG	GTGGAGGAAG	GGCCACCGA	ACAGCTGTTT	TCCTCGCCGA	60
AGCATGCGGA	AACCGCCCCG	TACGTGCGCG	GACTGTGCGG	GGACGTCAAG	GACGCCAAGC	120
GCGGAAATTG	AAGAGCACAG	AAAGGTATGG	CCTGAAATT	CGTTTGCATA	CGCTGTTGGC	180
CGTGTGACCC	GCTGCGCCGC	TGCTGCTAGC	AGCGGCGGGC	TGTGCTGHA	AACCACCGAG	240
CGGTTCGCTT	GAAACGGGCG	CCGGCGCCCG	TACTGTGCGG	ACTACCCCGG	CGTGGTCCGC	300
GGTGACCTTG	GCGGAGACCG	GTAGCAGCCT	GCTCTACCGG	CTGTTCAACC	TGTGGGCTCC	360
GGCCTTTTAC	GAGAGGTATC	CGAACGTCAC	GATCACCGCT	CGGGGACCGG	GTTCTGGTGC	420
CGGATGCGCG	CAGGCGCGCG	CCGGGACGCT	CAACATTGGG	GCTTCGACCG	CCTATCTGTC	480
GGAAGTGAAT	ATGCGCGCGC	ACAAGGGGCT	GATGAACATC	GGCTAGCCA	TCTCGCTCA	540
GCAGTCAAC	TACAACCTGC	CGGAGTGAAG	CGAGCACCTC	AAGCTGAACG	GAAAAGTCTT	600
GGCGGCGATG	TACCAGGCGA	CCATCAAAAC	CTGGGACGAC	CCGCAGATCG	CTGCGCTCAA	660
CCCGGGCGTG	AACCTGCCCC	GCACCGCGCT	AGTTCCGCTG	CACCGCTCCG	ACGGGTCCCG	720
TCACACCTTC	TTGTTCACCC	AGTACCTGTC	CAAGCAAGAT	CCCGAGGGCT	GGGSCAAGTC	780
GCCCGGCTTC	GGCACCACCG	TGAGCTTCCG	GGCGGTGCGG	GGTGGCTCGG	GTGAGAACCG	840
CAACGGCGGC	ATGCTGACCG	GTGCGGCCGA	GACACCGGGC	TGCGTGGCTT	ATATCGGCAT	900
CAGCTTCCTC	GACCGGCGCA	GTCAACGGGG	ACTCGGCGAG	GCCCACTAG	GCAATAGCTC	960
TGGCAATTTC	TTGTTGCCCC	ACGCGCAAG	CATTGAGGCT	GCGGCGGCTG	GCTTGGCATC	1020
GAAAACCCCG	GCGAACCAGG	CGATTTCGAT	GATCGACGGG	CCCGCCCCCG	ACGGCTACCC	1080
GATCATCAAC	TACGAGTACG	CCATGTTCAA	CAACCGGCAA	AAGGACGCGG	CCACCGCGCA	1140
GACCTTGCAG	GCATTTCTGC	ACTGGGCGAT	CACCGACGGC	AACAAGGCTT	CGTTCTCTGA	1200
CCAGGTTTAT	TTCCAGCCCG	TGCGGCCCCG	GGTGGTGAAG	TTGTCTGACG	CGTTGATCGC	1260
GACGATTTCG	AGCTAGCCCT	GTGACCACCG	ACGGACAGCG	AACCTCCGTC	GGGCCATCGG	1320
GCTGCTTTTC	GGAGCATGCT	GGCCCGTGCC	GGTGAAGTCC	GCCGCGCTCG	CCCGGCCATC	1380
CGGTGGTTGG	GTGGGATAGG	TGCGGTGATC	CCGCTGCTTG	CGCTGGTCTT	GGTGGTGGTG	1440
GTGCTGGTCA	TGAGGCGGAT	GGGTGCGATC	AGGCTCAACG	GGTTCGATTT	CTTACCGGCC	1500
ACCGAATGGA	ATCCAGGCAA	CACCTACGGC	GAAACCGTTG	TCACCGACCG	GTGCGCCATC	1560
CGGTGGGGCG	CTACTACGGG	GCCTTGCCCG	TGATGCTCGG	GACGCTGGCG	ACCTCGGCAA	1620

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TCGCCCTGAT CATCGCGGTG CCGGTCTCTG TAGGAGCGGC GCTGCTGATC GTGGACCGGC      1680
TGCGGAACG GTTGGCCGAG GCTGTGGGAA TAGTCTGGA ATTGCTCGCC GGAATCCCCA      1740
GCGTGCTCTT CCGTTTGTGG GGGGCAATGA CGTTCGGGCC GTTCATCGCT CATCATCG      1800
CTCCGGTGAAT CGCTCACAAC GCTCCGATG TCCCGGTGCT GAACACTTG CCGGGGACCC      1860
CGGGCAACGG GGAGGGCATG TTGGTGTCCG GTCTGGTGTT GGCGGTGATG GTCGTTCCCA      1920
TTATCGCCAC CACCACTCAT GACCTGTTC GGCAGGTGCC GGTGTTGCCC CCGGAGGGCG      1980
CGATCGGGAA TTC                                          1993

```

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:155:

```

Met Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro
1           5           10           15

Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
20           25           30

Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
35           40           45

Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
50           55           60

Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
65           70           75           80

Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
85           90           95

Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
100          105          110

Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
115          120          125

Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys
130          135          140

Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr
145          150          155          160

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Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
 165 170 175
 Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
 180 185 190
 Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly
 195 200 205
 Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly
 210 215 220
 Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
 225 230 235 240
 Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala
 245 250 255
 Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn
 260 265 270
 Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Gly Phe
 275 280 285
 Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro
 290 295 300
 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
 305 310 315 320
 Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
 325 330 335
 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val
 340 345 350
 His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
 355 360 365
 Ile Ala Thr Ile Ser Ser
 370

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GGTCTTGACC ACCACCTGGG TGTGGAAGTC GGTGCCCCGA TTGAAGTCCA GGTACTCGTG 60
 GGTGGGGCGG GCGAAACAAT AGCGACAGGC ATGCGAGCAG CCGCGGTATC CGTTGACGGT 120

GTAGCGAAAC	GGCAACGCCG	CCGCGTTGGG	CACCTTGTTC	AGCGCTGATT	TGCACACAC	180
CTCGTGAAG	GTGATGCCGT	CGAATTGTGG	CGCGCGAAGG	CTGCGGACCA	GGCCGATCCG	240
CTGCAACCCG	GCAGCGCCCG	TGCTCAACCG	GCATCCCGTT	CACCGCGACG	GCTTGCCCGG	300
CCCAACGCAT	ACCATATTTC	GAACAACCGT	TCTATACTTT	GTCAACGCTG	GCCTGTACCG	360
AGCGCCGCAC	AGGATGTGAT	ATGCCATCTC	TGCCCGCACA	GACAGGAGCC	AGGCCTTATG	420
ACAGCATTCG	GCGTCGAGCC	CTACCGGCAG	CGAAGTACC	TAGAAATCGC	CGGGAAGGCG	480
ATGCGGTATA	TGACGAAGG	CAAGGGTGAC	GCCATGCTCT	TTCAGCACCG	CAACCCACG	540
TGCTCTTACT	TGTGGCGCAA	CATCATGCGG	CCTTGGGAAG	GGCTGGGCGG	GCTGGTGGCC	600
TGCGATCTGA	TGGGATGCG	CGCTCGGAC	AAGCTCAGCC	CATCGGGACC	CGACCGTAT	660
AGCTATGCGG	AGCAACGAGA	CTTTTGTGTC	CGGCTCTGGG	ATGCGCTCGA	CCTCGGCGAC	720
CACGTGGTAC	TGGTGTGCA	CGACTGGGCG	TGGCGGCTCG	GCTTCGACTG	GGCTAACCGG	780
CATCGCGACC	GAGTGCAGGG	GATCGCGTTC	ATGGAAGCGA	TGCTCACCCC	GATGACGTGG	840
GGCGACTGCG	CGCCGGCCGT	GGGGGGTGTG	TTCCAGGGTT	TCCGATCGCC	TCAAGGGGAG	900
CCAATGGCGT	TGGAGCACAA	CATCTTTGTC	GAACGGGTGC	TGCCCCGGGC	GATCCTCGGA	960
CAGCTCAGCG	ACGAGGAAAT	GAACCACTAT	CGCGCGCCAT	TGCTGAACCG	CGCGCAGGAC	1020
CGTGGCCCCA	CCTTGTGCTG	GCCACGAAAC	CTTCCAATCG	ACGGTGAGCC	CGCCGAGGTC	1080
GTGCGGTTGG	TCAACGAGTA	CGCGAGCTGG	CTCGAGGAAA	CCGACATGCC	GAAACTGTTC	1140
ATCAACGCGG	AGCCCGGGCG	GATCATCACC	GGCCGCATCC	GTEACTATGT	CAGGAGCTGG	1200
CCCAACGAGA	CGAATACAC	AGTGGCCGCG	GTGCATTTCC	TTCAAGGAGG	CAGCGATGCG	1260
GTGCTATCGT	GGCGGGGCGC	TGGCAGCAT	CGCGGACCTG	GGAGCGCTCT	CATTTACCGA	1320
GACCAAGCAT	GTGATTTCCG	GCGAAGGCGG	CGCCCTGCTT	GTCAACTCAT	AAGACTTCTT	1380
GCTCCGGGCA	GAGATTCTCA	GGGAAAAGGG	CAGCAATCGC	AGCCGCTTCC	TTCCGAACGA	1440
GGTCGACAAA	TATACGTGGC	AGGACAAAGG	TCTTCTTATT	TGCCCAGCGA	ATTAATCGCT	1500
GCCTTTCTAT	GGGTCAGTT	CGAGGAAGCC	GAGCGGATCA	CGCTATCCG	ATTGGACCTA	1560
TGGAACCGGT	ATCATGAAAG	CTTCGAATCA	TTGGAACAGC	GGGGCTTCTT	GCGCCGTCTG	1620
ATCATGCCAC	AGGGCTGCTC	TCACAACGCG	CACATGTACT	AGTGTTACT	AGCGCCGAGC	1680
GCCGATCGGG	AGGAGGTGCT	GCGCGTCTG	ACGAGCGAAG	GTATAGGCGC	GCTCTTTCAT	1740

TACGTGCCCGC TTCACGATTC GCCGGCCGGG COTCCCT

1777

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GAGATTGAAT CGTACCGGTC TCCTTAGCGG CTCCTCCCG TGAATGCCCA TATCACGCAC 60
 GGCCATGTTT TGGCTGTGGA CTTTCGCCCC ATCCCCCGAC GTTGGTAAAC CCAGGTTTTC 120
 ATCAGTAATT CCGGGGAGCG GTTTCGGGAA GCGGCCAGG ATGTGCGTGA GCGCGCGCGC 180
 CGCGTCGCG CAGGCGACCG CTGGATGCTC AGCCCCGGTG CCGCGACTTA GCCAGCTTTT 240
 GGCGCGTGTG GTCCACAGTG GTACTCGGCT GACGACGCG CCGGCTGCTT GGGTGAAGAC 300
 CBTGACCGAC GCCGCGGATT CAGA 324

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

GCGGTACCGC CGCCTTCCCG TGGCAGGGA CCTGTACGAC CTGAACCACT TCGCCTCGCG 60
 AACGATTGAC GAACCGCTCG TCGCGCGCT GTGGTCTCTC AAGGTGTGGG GTGATGTCT 120
 CGATGACCGG CGCGGCACCC GCGCACTAG CTTCCAGAC GTCCCTCGCG CCGCGACGGA 180
 GCACGACTTC CAGCCCGACT CGATCGGCTT GCTGACCCGT CCTGTGCTA TGGCTGCTG 240
 GGAAGCTCGC GTTCGGAAGC GATTTGCTT CTTCACTGAC CTCGACGCG ACCGACGCG 300
 GTGGGCGCGC TGGACGAAC GGCACCGCG CGAAGTGGAG AACCGCTGG CGGTGCTGCG 360
 GTCCTGATCA ACCTGCGCGC GATCGTGGG TTCCGCTGGC ACGGTTGCGG CTGGACGCG 420
 CTGAATCGAC TAGATGAGG CAGTTGGGCA CGAATCGGC TGTGTTGTT AGCAAGACAC 480
 GAGTACTGTC ATCACTATTG GATGCACTGG ATGACCGGCT TGATTCAGCA GGACCAATGG 540
 AACTGCCCCG GGCAGAACCT CTCGAGATG ATCGGCTCC CCTCGGACC CTGCGGTGCT 600
 GGCGTCATTC GGACATCGCT CCGGCTCGCG GGATCGTGGT GACGCGAGG CTCGAGGAGT 660

```

GGAGCGCGGC GGTGCACGCG CTGCTGGACG GCCGGCAGAC GGTGCTGCTG CGTAAGGGCG 720
GGATCGGCGA GAAGCGCTTC GAGGTGGCGG CCCACGAGTT CTGTGTGTTT CCGACGGTGG 780
CGCACAGCCA CCGCGAGCGG GTTCGCCCCG AGCAGTGGCA CTTGCTGGGC CCGCGCGCGG 840
CGCACAGCAC CGACGAGTGT GTGCTACTGC GGGCGCGAGC GAAAGTTGTT GCCGCACTGC 900
CGGTTAAGCG GCCAGAGGGT CTGGACGCCA TCGAGGATCT GCACATCTGG ACCGCGGAGT 960
CGGTGCGCGC CGACCGGCTC GACTTTGGGC CCAAGCACAA ACTGCGCGTC TTGTTGGTCT 1020
CGGCGATCCC GCTGGCCGAG CCGGTGCGGC TGGCGCGTAG GCGCGAGTAC GCGGTTGCA 1080
CCAGCTGGGT GCAGCTGCGG GTGACGCCGA CGTTGGCGGC GCGGCTGCAC GACGAGGCGG 1140
CGCTGGCGCA GGTGCGCGGC CCGGTGCGGC AGGCGGTGGG TTGACTGGGC GGCATCGCTT 1200
GGGTCTGAGC TGTACGCCCA GTCGGCGCTG CGAGTGATCT GTGTGCGGT CCGTCCCTGC 1260
TGGCTCAAT TGACGCGCGG GGCAACAGCA GCATTGCGG CGCCATCCTC CCGCGCGCGG 1320
GGGCGCACCG CTACAACC 1338

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(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

```

CGGCGCGCAC CGGCGGCACC GGCGGTACCG GCGGCAACCG CCGTGACGCC GCTGCTGTGG 60
TGGGCTTGGG CGGGAACGGC GACCTTGCTT TCGTGGCGG CAAAGGCGGT AACGCGGAA 120
TAGGTGGGGC CGCGGTGACA GGCGGGCTCG CCGGCGACCG CGGCACCGGC GGCAAGGTG 180
GCACCGGCGG TGCCGCGCGC GCGGCAACG AGCGCGGCG CACCGGCAAT CCGGCGGTA 240
AGGCGCGCGA CCGCGGGATC GCGGTGCGG GCGGGCGCG CCGCGCGCGC GGCACCGCA 300
ACGCGGCGCA TCGCGCAAC C 321

```

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```

GAAGACCCCG CCCCGCCATA TCGATCGGCT CGCCGACTAC TTTCGCCGAA CGTGCACGCG 60
GCGGCCTCGG GCTGATCATE ACCGGTGGCT ACGCGCCCAA CCGCACCGGA TGGCTGCTGC 120
CGTTCGCTTC CGAACTCCTC ACTTCGGGCG AAGCCCCGACG GCACCGCCGA ATCACCAGGG 180
CGGTCCACGA TTCGGGTGCA AAGATCCTGC TGCAAATCCT GCACGCCGGA CGCTACGCTT 240
ACCACCCACT TCGGTCAGC GCTTCGCCGA TCAAGGGGCT GATCACCCCG TTTCGTCCGC 300
GAGCACTATC GGCTCGCGGG GTCGAAGCGA CCATCGGCGA TTTCGCCGCG TCGGCGCAGT 360
TGGCCCGCGA TGGCGGCTAC GACGCGCTCG AAATCATGGG CAGCGAAGGG TATCTGCTCA 420
ATCAGTTTCT GCGCGCGCGC ACCACACAGC GCACCGACTC GTGGGCGCGC ACACCGGCCA 480
ACCGTCGCGG GT

```

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

```

Phe Ala Gln His Leu Val Glu Gly Asp Ala Val Glu Leu Trp Arg Ala
1           5           10           15
Asn Ala Ala Asp Gln Ala Asp Pro Leu Gln Pro Gly Ser Ala Arg Arg
20           25           30
Gln Arg Ala Ser Arg Ser Pro Arg Arg Leu Ala Gly Pro Asn Ala Tyr
35           40           45
His Tyr Ser Asn Asn Arg Ser Ile Leu Cys Gln Arg Trp Pro Leu Pro
50           55           60
Ser Ala Ala Gln Asp Val Ile Cys His Leu Cys Pro His Arg Gln Glu
65           70           75           80
Pro Gly Leu Met Thr Ala Phe Gly Val Glu Pro Tyr Gly Gln Pro Lys
85           90           95
Tyr Leu Gln Ile Ala Gly Lys Arg Met Ala Tyr Ile Asp Glu Gly Lys
100          105          110
Gly Asp Ala Ile Val Phe Gln His Gly Asn Pro Thr Ser Ser Tyr Leu
115          120          125
Trp Arg Asn Ile Met Pro His Leu Glu Gly Leu Gly Arg Leu Val Ala

```

160

130	135	140
Cys Asp Leu Ile Gly Met Gly Ala Ser Asp Lys Leu Ser Pro Ser Gly		
145	150	155
Pro Asp Arg Tyr Ser Tyr Gly Glu Gln Arg Asp Phe Leu Phe Ala Leu		
	165	170
Trp Asp Ala Leu Asp Leu Gly Asp His Val Val Leu Val Leu His Asp		
	180	185
Trp Gly Ser Ala Leu Gly Phe Asp Trp Ala Asn Gln His Arg Asp Arg		
	195	200
Val Gln Gly Ile Ala Phe Met Glu Ala Ile Val Thr Pro Met Thr Trp		
	210	215
Ala Asp Trp Pro Pro Ala Val Arg Gly Val Phe Gln Gly Phe Arg Ser		
	225	230
Pro Gln Gly Glu Pro Met Ala Leu Glu His Asn Ile Phe Val Glu Arg		
	245	250
Val Leu Pro Gly Ala Ile Leu Arg Gln Leu Ser Asp Glu Glu Met Asn		
	260	265
His Tyr Arg Arg Pro Phe Val Asn Gly Gly Glu Asp Arg Arg Pro Thr		
	275	280
Leu Ser Trp Pro Arg Asn Leu Pro Ile Asp Gly Glu Pro Ala Glu Val		
	290	295
Val Ala Leu Val Asn Glu Tyr Arg Ser Trp Leu Glu Glu Thr Asp Met		
	305	310
Pro Lys Leu Phe Ile Asn Ala Glu Pro Gly Ala Ile Ile Thr Gly Arg		
	325	330
Ile Arg Asp Tyr Val Arg Ser Trp Pro Asn Gln Thr Glu Ile Thr Val		
	340	345
Pro Gly Val His Phe Val Gln Glu Asp Ser Asp Gly Val Val Ser Trp		
	355	360
Ala Gly Ala Arg Gln His Arg Arg Pro Gly Ser Ala Leu Ile Ser Arg		
	370	375
Asp Gln Glu Cys Asp Phe Arg Arg Arg Arg Arg Pro Ala Cys Gln Leu		
	385	390
Ile Arg Leu Pro Ala Pro Gly Arg Asp Ser Gln Gly Lys Gly His Gln		
	405	410
Ser Gln Pro Leu Pro Ser Gln Arg Gly Arg Gln Ile Tyr Val Ala Gly		
	420	425

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Gln Arg Ser Ser Tyr Leu Pro Ser Glu Leu Val Ala Ala Phe Leu Trp
 435 440 445
 Ala Gln Phe Glu Glu Ala Glu Arg Ile Thr Arg Ile Arg Leu Asp Leu
 450 455 460
 Trp Asn Arg Tyr His Glu Ser Phe Glu Ser Leu Glu Gln Arg Gly Leu
 465 470 475 480
 Leu Arg Arg Pro Ile Ile Pro Gln Gly Cys Ser His Asn Ala His Met
 485 490 495
 Tyr Tyr Val Leu Leu Ala Pro Ser Ala Asp Arg Glu Glu Val Leu Ala
 500 505 510
 Arg Leu Thr Ser Glu Gly Ile Gly Ala Val Phe His Tyr Val Pro Leu
 515 520 525
 His Asp Ser Pro Ala Gly Arg Arg
 530 535

(2) INFORMATION FOR SEQ ID NO:162:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 284 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Asn Glu Ser Ala Pro Arg Ser Pro Met Leu Pro Ser Ala Arg Pro Arg
 1 5 10 15
 Tyr Asp Ala Ile Ala Val Leu Leu Asn Glu Met His Ala Gly His Cys
 20 25 30
 Asp Phe Gly Leu Val Gly Pro Ala Pro Asp Ile Val Thr Asp Ala Ala
 35 40 45
 Gly Asp Asp Arg Ala Gly Leu Gly Val Asp Glu Gln Phe Arg His Val
 50 55 60
 Gly Phe Leu Glu Pro Ala Pro Val Leu Val Asp Gln Arg Asp Asp Leu
 65 70 75 80
 Gly Gly Leu Thr Val Asp Trp Lys Val Ser Trp Pro Arg Gln Arg Gly
 85 90 95
 Ala Thr Val Leu Ala Ala Val His Glu Trp Pro Pro Ile Val Val His
 100 105 110
 Phe Leu Val Ala Glu Leu Ser Gln Asp Arg Pro Gly Gln His Pro Phe
 115 120 125

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Asp Lys Asp Val Val Leu Gln Arg His Trp Leu Ala Leu Arg Arg Ser	
130	140
Glu Thr Leu Glu His Thr Pro His Gly Arg Arg Pro Val Arg Pro Arg	
145	155
His Arg Gly Asp Asp Arg Phe His Glu Arg Asp Pro Leu His Ser Val	
165	175
Ala Met Leu Val Ser Pro Val Glu Ala Glu Arg Arg Ala Pro Val Val	
180	190
Gln His Glu Tyr His Val Val Ala Glu Val Glu Arg Ile Pro Glu Arg	
195	205
Glu Gln Lys Val Ser Leu Leu Ala Ile Ala Ile Ala Val Gly Ser Arg	
210	220
Trp Ala Glu Leu Val Arg Arg Ala His Pro Asp Gln Ile Ala Gly His	
225	240
Gln Pro Ala Gln Pro Phe Gln Val Arg His Asp Val Ala Pro Gln Val	
245	255
Arg Arg Arg Gly Val Ala Val Leu Lys Asp Asp Gly Val Thr Leu Ala	
260	270
Phe Val Asp Ile Arg His Ala Leu Pro Gly Asp Phe	
275	280

(3) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

ATGAACATGT CGTCGGTGGT GGTGCGCAAG GCCTTTCCGC GATTCGCCCG CTACTCCTCC	60
GCCATGCACG CCGTCGCCCG TTCTCCCAT GCCTTCCGCC AAGAGCTGCC CGGTAGCGGA	120
ATCGCCGTGT CGGTGATCCA CCGGGCCCTG ATCCAGACAC CGCTTTGGGC CAACCTCGAC	180
CCCGCCGACA TCGCGCCCGC GTTTCGCAGC CTCAGGCCCA TTCCCGTTCA CTGGGTCCCG	240
GCAGCGGTGC TTGACGGTGT GCGC	264

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1171 base pairs

163

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

TAGTCGGCGA CGATGACSTC GCGGTCCAGG CCGACCGCTT CAAGCACCAG CCGGACCACG	60
AAGCCGGTGC GATCCTTACC CCGGAACAG TGGGTGAGCA CCGGGCGTCC GCGGCAAGC	120
AGTGTGACGA CAGGATGTAG CCGCGCGTGT GCTCCATTTC GCGTTGGGAA TTGGCGATAC	180
TCGTGCGTCA TGTAGCGGCT GCGGCGCTCA TTTATCGACT GCGTGGATTC GCGGACTCG	240
CGCTTGGACC CCGATTGGT TAGCAGCCTC TTGAATCGCG TTTCGTCCCG CCGTGAAGTC	300
TCGGCGTCAT CATCGGCGAG GTGCGGGAAC GCGACGAGGT GCGCTCGAT CCGGTCCGGA	360
ACCGTCTCTG GACCGCGGCG GCGAACCTCC CCGGACGACC GCGGTCTGCG AACGTCTGTC	420
ATCGCCAGCC GCGCGAGCCT TCGCCCTCGT GCGGAATTCG GCACGAGCCT GCGGAGCCAC	480
CSSGCATCAC CAAGCAACGC TTGCCCAGTA CCGATCGTCA CTTCCGCATC CCGCAGACCA	540
ATCTCTTCGC CGCCCATCCT CAGATCCCGC TCGTGGGTTG ACAAGAACCG CCGCAGATGT	600
GCGAGCGGCT ATCGGAGATT GAACCGGCGA CCGATTCTT CAATCGCTGC GCGCTCGCGC	660
ACTATTGGCA CTTTCGCGCG GTCCCGGTAT TCAGCAAGCA TCGGACTCTC GACGACTCG	720
CCCCCGTAA CCGACGCGCT AGCTCCCGGC GTGACGCGGA GCGTCGCGCG GTGATCTTTG	780
CGCCACGCT CTTAGCGCTT GATCCAGCG TTCCCGGTGC CCGCGCGGAG GCGGATCAGC	840
TTATCGACCT CCGCGTATGC CGACGCGAAG CTGGGCGCGT TCGTCGAGGT CAAGAACTCC	900
ACCATCGGCA CCGGCACCAA GGTGCGGCGC CTGACCTAGC TCGCGGACGC CGACATCGGC	960
GAGTACAGCA ACATCGCGGC CTCGAGCGTG TTCTCAACT ACGACGGTAC GTCCAAACCG	1020
CGCACGCGCG TCGTTTCGCA CGTACCGACC GGTCCGACA CCGTGTTCGT GCGCCCGATA	1080
ACCATCGCGC ACGGCGCGTA TACCGCGGCG GGCACAGTGG TCGCGGAGGA TGTCCCGCGC	1140
GGGCGCGTGG CAGTGTGCGC GGTCCCGCAA C	1271

(2) INFORMATION FOR SEQ ID NO:165:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GCAAAGGCGG CACCGGCGGG GCGGGCATGA ACAGGCTCGA CCGGCTGCTA GCGGCGGAG	60
ACGGCGGCGA AGGGCGGCGG GCGGGGACCG GCGGCAACGC CCGGCGGCGG GGCACCGCT	120
TCACCCAAAG GCGGACCGG AACGCGGCGA ACGGCGGTGA CCGGCGGCTC GCGGCGGAG	180
GCGGAAAGCG CGGAAACGCG GCAGACAACA CCACGACCGG CCGGCGG	227

(2) INFORMATION FOR SEQ ID NO:166:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

CCTCGCCACC ATGGGCGGGC AGGCGGCTAG CGGTGCGGCG GCTCTACCC CAGGCGGAA	60
GGGCGGCGAC GCTTCACTC CAACGAGCGG CCGCGACGCG GCGGACGCGG GCAACGCGG	120
CAACTGCGAA GTGGTCGGCG GCAACGCGG CGACGCGGCG AATGCGGCGA ACCGCGGCG	180
CGCGGCGAGG GCGGCGAGCG GCGGCGGCG GCGGACGCG GCTTTTGGTG GCATGAGTC	240
CAACGCGACC AACGCTGGTG AAAACGCGCG AAACGCTAAC CCGGCGGCGA ACCGTCGCG	300
CGGC	304

(2) INFORMATION FOR SEQ ID NO:167:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GTGGGACGCT GCGGAGGCTG TATAACAGG ACAACATCGA CCAGCGCGCG CTGGTGAAG	60
TGATGACGCT ATTAAACAGT GCGCGCTTCA GCGGCGAGGG CGAGCAGCGG GCGCGGATC	120
TGATGGGTGA GGTCTACGAA TACTTCTCTG GCAATTTCGC TCAGCGCGAA GCGAAGCGGG	180
GTGGCGAGTT CTTACCGCG CCGAGGCTGG TCAAGGTGAT CGTGCAGGTG CTGGAGCGCT	240
CGAGTGGCGG GGTGTATGAC CGTCTCTCGG GTTCGCGAGG CATGTTTGTG CAGACCGAGA	300
AGTTCACTTA CGAACAGGAC GCGGATCGGA AGGATGTCTC GATCTATGCG CAGGAAAGCA	360
TTAGAGAGAC CTGGCGGATG GCGAAGATGA ACTTGGGCTT CCAGGCGATC GACAACAGG	420

GGCTCGGCGC CCGATGGAGT GATACCTTCG CCGCGACCA GCACCCGGAC GTCCAGATGG	480
ACTAGTGTAT GGCCTATCCG CCGTTCRACA TCAAAGACTG GGGCCGCIAC GAGGAAGACC	540
CACGCTGGCG CTTCGCTGTT CCGCCCGCCA ATAACGCCAA CTACCGCATGG ATTACGACAA	600
TCTGTACAA CTTCGCGCCG GAGGTCCGG CCGGCGTGGT GATGCGCAAC GGTTCGATGT	660
CGTCGAATTC CAACGCAAG GGGGATATTC GCGCGCAAT CGTCGAGCGG GATTCGTTTT	720
CTTCGATGGT CGCTTACCC ACCGAGCTGT TCCGAGCAC CGGAATCCCG GTGTGCTTGT	780
GGTTTTTCGC CAAAAACAAG GCGGCAGGTA AGCAAGGTC TATCAACCGG TCGCGCAGG	840
TCTGTGTAT GAGCGCTGCT GAACTGGGCG ACCTAGTGA CCGGGCCGAG CCGGCGCTGA	900
CCAACGAGGA GATCGTCCGC ATCGGGGATA CTTTCCACGC GAGCACGACC ACCGCGAAGC	960
CGGCTCCCG TGGTCCCGGC GTTAATGGGG GCACTGGCTT CAACCGCGCG GCGGCTGCTG	1020
GCGGGGCGCG CGGCAACCGG GTGTCCCGG GCTGTCTCTT CGGCAACGCT GTGGGCGGCG	1080
ACGGGGGCAA CCGCGGCAAC GCGGGCCAG GCGGCGACG CACGACGGGC GCGGCGGCG	1140
GCAAGGGCGG CAACGCGAG AGCGTGGCG CCGCGGCTC AGGCTGCTC AACGTCAAGG	1200
CGGCGACCG CGGCAACGCG GCGATGCGG GCAACGCGG CAACGCTCT GCGGCGGCG	1260
GCGGCGACCG CGGTCCCGG GCGAGCGCG GCAACGCGG CACGCGGCG GGTGCCACCG	1320
GCGGCGGCG CGGCAAGGCG GCGACGCGA CCGCGGTC GCGGCGGCG TCAGGCTCA	1380
TCAACGTCAC CCGCGGCGC GCGGCAAG GCGGCAATGG CCGCAACGCG GCGAAGCG	1440

(2) INFORMATION FOR SEQ ID NO:168:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 129 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GGGCGGCGG GCGCGATTT TCTGTGCTT TGATTGTGC TGGGATAAC GCGGCTGATG	60
GTGGTAACCG CCGGATGGGC GGGGCTGGCG GGGCTGGCG CCGCGCGCG GCGGCGGCG	120
TGATCAGCTT GCTGGGCGCG CAAGGCGCG GCGGCGCGG CCGGACCGG GCGGCGGCG	180
GTGTGGCGG TGAAGGCGG GCGGCGGCG CCGGCAACCA GCGCTTCAAC GAGGTGCGG	240
GCGGCGGCG CCGGCTGATC AGCTGCTGG GCGGCAAGG CCGGCGGCG GCGGCGGCG	300
CAGGCGGCG CCGGCTGTT GCGGCTGAC	329

(2) INFORMATION FOR SEQ ID NO:169:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GCAACGGTGG CAACGGCGGC ACCAGCACGA CCGTGGGGAT GCGCGAGGT AACTGTGGTG 50
 CCGCGGGGCT GATCGGCAAC 80

(2) INFORMATION FOR SEQ ID NO:170:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 392 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

GGGCTGTGTC GCACTCACAC CGCCGATTG GCGAGCTTG GCGGCCCAAT ATCCAGCTCA 50
 AGGCTTACTA CTTACCGTGG GAGGACCGCC GCATCAAGGT GCGGGTCAGC GCGCAAGGAA 100
 TCAAGGTGAT CGACCGCGAC GCGCATCGAG GCGGTCTGCG CGCGGCTCGG GCAGGATCCG 150
 CCGCGGCGCA CTTGCGCGCG CAAGCGGCT CATCGCTCG AAGCGCGCG ATCTGTGAG 200
 CACAAGTAT GCGCGCGAAC GAGATTCGTC CAATTGTGAA GCGGTGTCG ACCGAGGGA 250
 CCGGTTATAC GTATGTCAAC CTATGTCAT CGCAAGAACC GGCATACGA TCCCGTGATC 300
 CGGCGACAGC CCACGAGTGC AAGACCGTTC CA 350
 392

(2) INFORMATION FOR SEQ ID NO:171:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

ACCGCGGCGA CCGCGCGCAC CCGGTTGCGC GGTGCGCGCG GCGCGCGCGG CCGGCAGGCG 50
 GTATTCAGCG GTGCGCGCGG CACCAACGCG TCTGCTGGCG CTGCGCGCAC CCGCGGACAA 100
 GCGCGCGCGG GCGCGCGTGG CCGCGCGCGG GCGGATAACC CCACCGCAT CCGCGCGCGG 150
 335

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GGCGGCACCG	GGGSCACCGG	CGGAGCGGCG	GGAGCGGGCG	GGGCGGGTGG	CGCCATCGGT	240
ACCGGCGGCA	CGGCGGCGCG	GGTGGGCAGC	GTGGGTAAAG	CGGGATCGG	CGGTACCGGC	300
GGTACGGGTG	GTGTGGGTGG	TGCTGGTGGT	GCAGGTGCGG	CTGGGGCCGC	TGGCAGCAGC	360
GCTACCGGTG	GGGCGGGGTT	CGCGGGCGGC	GCCGGCGGAG	AAGGCGGACC	GGGCGGCAAC	420
AGCGGTGTGG	GGGCGACCAA	CGGTGCGGCG	GGCGCGGGCG	GTGCAGGGCG	CAAGGCGCGC	480
ACCGGAGGTG	CGGCGGGGTC	CGGCGGCGAC	AACCGCACCG	GTGCTGGTTT	CGCGG	539

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

CCGACGTGGC	CGGGGCGATA	CGGGGGTCAC	CGACTACTAC	ATCATCCGCA	CGGAGAATCG	60
GGCGGTGGTG	CAACCGCTGC	GGGCGGTGCC	GGTCATCGGA	GATCGGCTGG	CGGACCTGAT	120
CCAGCGGAAC	CTGAAGGTGA	TGGTCAACCT	GGGCTACGGC	GACCGGAATC	ACGGCTACTC	180
GACGAGCTAC	GGCGATGTGC	GAACGCGGTT	CGGGGTGTGG	CGGAACCTGC	CGGCTCAGGT	240
CATCGCGGAT	GGGCTGGGCG	CGGGAACACA	AGAAGGCATC	CTTGACTTCA	CGGCGGACCT	300
GCAGGGGCTG	TGGCGGCAAC	CGGTCAGGCT	CGGCGAGATC	CAGCTGGGCG	AACCGGCGCA	360
TGTGGTGGGC	GGGGTGGGCG	CGGCACCGAC	GCGGGCGGAG	GTGGTGAACA	CGGTCGGCAG	420
GATCATCTCA	ACCAACTAGG	CGGCTGTGCT	GCGGACCGTG	GACATCGGCG	TGGGCTGGTC	480
ACCAGCGTGC	CGGTGTACAC	CAGCGAAGTG	TTGGTCAGGC	AACTCGCTGC	GGGCAATCTG	540
ATCAACGGCA	TGGGCTATCC	CGTGGGGGCG	ACCGTAGGTT	TAGGCAAGAT	CGTAGCGGGG	600
CGGGGTGGAA	TTGCTCACCC	TGCTGCGGCG	GGGCTCGGAC	ACCGTTGCAA	ACATCGAGGG	660
CGTGGTCACC	TAAAGGATTC	CGGACGGCAT				690

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

```

ACGGTGACCG CGGTACTGSC GCGGCCCACG GCGGCAACCG CGGGAATCCC GGGTGGCTCT 60
TGGGCACAGC CGGGGGTGGC GSCAACGGTG GCGCCGSCAG CACCGGTACT GCAGGTGGCG 120
GCTCTGGGGG CACCGGCGGC GACGCGGGGA CCGCGGGCGG TGGCGGCTTG TTAATGGGCG 180
CGGCGCGCGG CGGGCACGGT GCACTGGCG GCGCGGGCGG TGCGGGTGTG GACGGTGGCG 240
GGCGCGGGCG GCGCGGGCG GCGCGGGCGA ACGCGGGCGC CGGGGGTCAA GCGCGCTTC 300
TGTTCGGGCG CGGCGGCACC GCGCGAGCGG GCGGCTACCG CGGCGATGCC GGTGGCGGCG 360
GTGACGGCTT CGACGGCAGG ATGCGCGGCG TGCGTGGTAC CGGTGGC 407

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(2) INFORMATION FOR SEQ ID NO:174:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 468 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

```

GATCGGTGAG CGCATCGCCG TCGCGGCGAA GCGATTCCGC GGTCTCACCG AAGAACATCG 60
TGCACGCGCG GCGCGGAGC AGCCCGGTGC GCTGCGGCGC GTCGAACGCC TCCAGCAGGC 120
ACAGCCAGTC CTTGGCGGCG TCGAGGCGGA ACAGGTGGGT GTCACCGGTG TAGATCGCGG 180
GGATGCGGCG CTCGCGCAAC GCATTCCGGC ACGCGCGCGC GTCTTTGTGA TGCTCGACGA 240
TCACGCGGAT GTCTCGGCG ACCACGGGCG GCGCGCGCAA GGTGGCGCGG CTGCGCAGTA 300
GCGCGCGGAC GTGCGCGGCG AGGTGGTCGG GGATGTGCGG GCGCAGCGCT CCGGCGCGAC 360
GCGCGAAAAA CGACCGCTCA CCGAGCTGGG TCGCGGTGGC ATATCCCTTG CCGTCTCTGG 420
CGATATTGGA CGCGCATGCC CCGACCGCGT ACAGCGCGCG CACTACCG 468

```

(2) INFORMATION FOR SEQ ID NO:175:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

```

GGTGGTAACG GCGGCGAGCG TGCGATCGCG GCGCGCGGCG AGAGAGGCGC CGACCGCGCG 60
GGCGCGCATG CTAACCGCGC AAACGGCGAG AACGGCGGTA GCGGTGGTAA CCGTGGCGAC 120

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GGCGGCGCCG GCGGCATGG GCGCGCGGCG GGCACCGCG AGGCGGCGCG GTACACCGAC 180
 GCGGCCACGG GCACCGCGCG CGACGGCGCG AACCGCGCG 219

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

TAGCTCCGGC GAGGCGCGCA AGGCGCGCGA CGGTGGCCAC GGCGGTGACC GCTTCGGCGG 60
 CAACASTTCC CTCACCCCAAG GCGGCAGCGG CGGTGGCGCG GCGCGCGCGG GCGCGCGCGG 120
 CAGCGGCTTT TTGCGCGGCA AGGCGCGCTT CGGCGCGCAC GCGCGTCAGG GCGCGGCTTA 180
 CGGCGCGCGT ACCGTCCGCA CCGTGGCGCG TGGCGCGCGC AACCGCGCGT TCGCGCGCGG 240
 GCGCGCGCGAC GCGGTCTTTG CCGGTGGCGG CGGCGCGCGC GCGCTCGGTG GCGAGGGCGG 300
 CAATGCGCGC GCTTCACCG GCGCAACGG CGGCTTGGC GCGCGCGCGG GTGGCGGAGG 360
 CAACGCGCGG GCTCGTCCG AATCGCGGCT GACCATGGAC AGCGCGGCGA AGTTCGCTGC 420
 CATCGCATCA GCGCGTACT GCGCGGACCA CTTGGACAT CACCGGAGTT AGCGGGGTCG 480
 ATTTCTTGAT CACT 494

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GGGCGGCTGG TCGCGCGCGC CAGCTCTTCA GCGCGGAGG CGCGCGCGGT GCGCTTGGG 60
 TTGGCGGAC CCGCGGCGCG GTGGCGGCTG GCGGTCCCG AGCGCGCGCG GCGGACGCGG 120
 CGGCGGCGAC AGGTCTAACC GTGGTACCG GTTTCGCTGG CGGCGCGCGC GCGGTCCGCG 180
 GCGAGGCGG CAACGCGATT GCGCGCGCGA TCAACGCTC 220

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

ATGGCGGCAA CCGGGGCTCC GCGGGTGCTG GCGGGGCGGG CGACTACAAT TTCCAACGGC	60
GGGCAGGCTG GTCCCGCGGG CCAAGGCGGG CAAGGCGGGC TGGGCGGGGC AAGCACCACC	120
TGATCGGCTT AGCGGCACCT GGGAAAGCGG ATCCACAGG CGACGATCC GCCTTCCTTG	180
CCCGTTTGA CCGGGCGGG ATCACTTACC CTGACCCAGG CCACGCCATA ACGGCCCCCA	240
AGGCGATGTG TGGGTGTGT GCTAACGGG TACAGGTCT ACAGCTGGTC GCGGACTTGC	300
GGGACTACAA TCCCGGCTG ACCATGACA GCGCGGCCAA GTTCGCTGCC ATCGCATCAG	360
GCGGCTACTG CCCCAGACAT CTGGAACA	388

(2) INFORMATION FOR SEQ ID NO:178:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GCAAAGGGGG CACCGGCGGG GCGGGCATGA ACGGCTTCCA CCGGCTGCTA GCGGGCCAG	60
ACGGCGGCCA AGGGCGGAGC GCGGGCACCG GCGGCAAGGC CCGCGCGGGC GGCACCACT	120
TCACCCAGAG CCGGACGGC AACCTTGGCA ACGCGGCTGA CCGCGGGGTC GCGGGCAAGC	180
GCGGAACCGG CGGAACGGC GCAGACAACA CCGCACCGGC CGCGGCGGGC ACCACAGGGC	240
GGGACGGCGG GCGCGGGGG GCGGCGGAA CCGGCGGAAC CGGCGGAGCC GCGGGCACCG	300
GCACCGCGGG CCAACAAGGC AACGGCGGCA ACGGCGGCAC CCGGCGGAAA GCGGGCACCG	360
GCGGCGACCG TGCATCTCA GCGAGCACCG GTGGTCCCGG	400

(2) INFORMATION FOR SEQ ID NO:180:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 538 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GGCACCGCG GCAACGGCG CATCGCTGGC ATTGGGCGGC AACGGCTTC GGGGACGGGC	60
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AGCGGCAACG GCGGCTCAACG GCGGCAGCGG CGGCAACGGC GGCACGCGG GCATGCGCGG	120
CAACAGCGGG ACCGGCAAGG GCGACGGCGG TGCCGGCGGG AACGGCGGGG CGGCGGCGAC	180
GGGCGGCACC GCGGCGGACG GCGGCTTCAC CGGTACTGGC GGCACCGGGG GCAGCGGTGG	240
CACCGGCGGT GACGGCGGTA ACCGGCGCAA CGGAGCAGAT AACACCGCAA ACATGACTGC	300
GCAGGCGGGC GTGACGGTG GCAACGGCGG CGACGGTGGC TTCGGCGGGG GGGCGGCGGC	360
CGGCGGCGGT GGTGTGACCG CTGGCGCCAA CGGCACCGGC GGGCAAGGGG GCGCGGCGGG	420
CGATGCGGGC AACGGGCGCA TCGCGCGCCA CGGCGCACTC ACTGACGACC CCGCGGCGCA	480
CGGCGGCAAC GCGGCAACG GCGGCACGGG CGGCACCGGC GCGCGGCGCA TCGGCGGC	538

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 238 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

GGGCGGCGTG TGCGCGGGGC CAGCTCTTCA GCGCGGAGG CGCGGCGGT GCGTTGGGG	60
TTCGCGCAC CGCGGCGCAG GTGCGGCTG GCGGTGCGG AGCGGCGGG GCGACGCGC	120
CGGCGGCGC AGGTCTAACC GGTGTACCG GTTGTGCTG CGCGGCGGG GCGTTCGCG	180
GCTACGCGG CAACGCCATT GCGGCGGCA TCAACGGCT CGGTGCTGC GCGGCGAC	238

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 368 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

AGCAGCGCTA CCGGTGCGGC CGGTTGCGC GCGGCGGCG GCGGAGAGG CGGAGCGGC	60
GCGACAGCG GTGTGGGCG CACCAACGGC TCGGCGGGG CGGCGGTGC AGCGGCGAAG	120
GGGCGCACCG GAGTGCCTG CGGTCGCGC TCGGACAAAC CCACCGGTG TGGTTTGGC	180
GGTGGCGCGG GCGGCACAG TGGCGGGGC GCGCGCGCG GCGGCGCGG GCGGACCGT	240
ACCGCGGCA CCGCGCGGT TGTGCGGCG ACCGTAGTG CAGGCATCG CGGCGCGGC	300
GGGCGCGGG GTACCGCGG CAGTGGGCG AGCGTCTCG GCGTGGGCT CTCGCGTTT	360

GACGCGCGCC AAGGCGGCCA AGGCGGGGCC GCGCGCAGCG CCGCGCGCGG CCGCATCAAC	420
GGGCGCGGCG GGGCGGCGCG CAACGGCGGC GACGCGCGGG ACGCGCGAAC CGGTGCGGCA	480
GCTGTGCGCG ACAACGCGCG GGTGCGCGGT GACGCGGGGG CCGGTGCGCG CCGCGGCAAC	540
GGCGGCAACG CCGGCGTGGG CCGGACAGCC AAGGCGGGCG ACGCGCGCGC CCGCGGCAAT	600
GGCGGCAACG GGGGCGCGCG CCGTGCTGGC GGGCGGCGCG ACAACAATTT CAACGGCGGC	660
CAGGCTGGTG CCGCGCGCCA AGGCGGCGCA GCGCGCTTGG GCGGGGCAAG CACCACTTGA	720
TGGGCGTAGC CCGACCGCGG AAAGCGGATC CAACAGGCGA CGATGCGCGC TTCCTTGGCG	780
CGTTGGACCA GCGCGGATC ACCTACGCTG ACCGAGGCGA CGCATAACG GCGCGCAAGG	840
CGATGTGTGG GCTGTGTGCT AACGCGCTAA CAGGTGTACA GCTGCTCGCG GACCTGCGCG	900
AATACAAATC CCGGCTGAGC ATGGACAGCG CCGCGAAGTT CCGTGGCATC GCATCAGGCG	960
CGTACTGCGC CGAACACCTG GAACA	985

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2138 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

CGGCAGGAGG ATCGGTACCC CCGCGCATCG GCAGCTGCGG ATTGCGCGGG TTTCGCCACC	60
CGAGGAAGG CGTACCAGA TGGCGTGGC GAAGTAGGCG GATCGCTTGG CGATGCGCGC	120
ATGAACGGGC GGCATCAAT TACTGCAGGA ACCTTTCAAT TTAGCGACGA TAATGGCTAT	180
AGCACTAAGG AGGATGATCC GATATGACCG AGTCGACAGC CCGTACGCTG GATCAGCAAG	240
AGATTTTGAA CAGGCGCAAC GAGGTGGAGG CCGCGATGGC GGATCCACCG ACTGATGTCC	300
CCATCACACC GTCCGAATTC ACGGCGGCTA AAAACGCGCG CCAACAGCTG GTATTGTCCG	360
CGACAAATAT GCGGGAATAC CTGGCGGCGG GTGCCAAGA GCGGAGCGGT CTGGCGACCT	420
CGCTGCGCAA CGCGGCAAG GCGTATGGCG AGGTTGATGA GGAGGCTGGG ACCGCGCTGG	480
ACAAGGACCG CGAAGGAAT GTCCAGGCAG AATCGCGCGG GCGGCTCGGA GGGGACAGTT	540
CGGCGGAAT AACCGATAC CCGAGGCTGG CCACGCGCGG TGAACCGAAC TTCATGATC	600
TCAAAGAAGC GGCAGGAAG CTCGAACCGG GCGACCAAGG GGCATCGCTC GCGCACTTTC	660

CGGATGGGTG GAACACTTTC AACTTGACGC TGCAGGCGCA COTCAAGCGG TTCCGGGGGT	720
TTGACAACTG GGAAGGCGAT GCGGCTACCG CTTCGGAGGC TTCCCTCGAT CAACAACCGC	780
AATGGATACT CCACATGGCC AAATTEAGCG CTGGGATGGC CAGCAGGCT CAATATGTGG	840
CGCAGCTGCA COTGTGGCT AGGCGGGAAC ATCCGACTTA TGAAGACATA GTCCGGCTCG	900
AACGGCTTTA CCGGAAAC CCTTCGGCC GCGACCAAT TCTCCGGTG TACCGGGAGT	960
ATCAGCAGAG GTCCGAGAG GTGCTGACCG AATACAACAA CAGGCAGCC CTGGAACCGG	1020
TAAACCCCGC GAAGCCTCCC CCGCCATCA AGATCGACCC GCGCCGGCT CCGCAAGAGC	1080
AGGGATTGAT CCGTGGCTTC CTGATGCGGC COTCTGACCG CTCGGGTGTG ACTCCGGTA	1140
CGGGATGCC AGCCGCACCG ATGCTTCGCG CTACCGGATC GCGGGTGGT GCGCTCCCGG	1200
CTGACAGGCG GCGCAGCTG ACCTCGGCTG GCGCGGAAGC CCGAGGCTG TCGGCGAGC	1260
TGGCGTCAA AGCGGATCG CTCGGTGGCG GTGAGCGCG GCGGTGCGG TCGGCGCGCT	1320
TGGGATCCC GATCGGGGCT GCGAATCGG TCGGCGCGCG TGGCGCTGGT GACATTGCGG	1380
GCTTAGGCCA GGAAGGGCC GCGGCGGCG CCGGCTGGG CCGCGGTGGC ATGGGAATGC	1440
CGATGGGTGC CCGCATCAG GACAAGGGG GCGCCAAGTC CAGGGTTCT CAGCAGGAG	1500
ACGAGGCGCT CTACACCGAG GATCGGGCAT GACCGAGGC GTTCATTGGT AACCTCGGC	1560
GCGAGACAG TAAGGACTCG AAGTACGAT GAGCAATTG GACTTCATG TCGCGCGGC	1620
GTGACCTG GCGCGCGCT TTCACTCGGC CTTAGACCGG ACGCTCAATC AGATGACAA	1680
CGGATCCTTC CCGCCACCG ACGAAGCGGA GACCTTCGAA GTGACGATCA ATGGGCACCA	1740
GTGGCTCACT GCGCTCGCA TCGAGATGG TTGCTGAAG AAGCTGGGTG CCGAGCGGT	1800
GGCTAGCGG GTCAACGAGG CGCTGCACAA TCGCAGGCG GCGCGTCCG COTATAACGA	1860
CGCGCGGCG GAGCAGCTGA CCGTCCGTT ATCGGCGATG TCGCGCGGA TGAACGAAGG	1920
AATGGCTTAA GCGATTGTT GCGGTGGTAG CGACTACGCA CCGAATGAGC GCGCAATGC	1980
GCTCATTCAG CCGCGCGGAC ACGCGTGGG TACGCTTGT CAATGTTTT ACATGGATCG	2040
GCGGGTTTG GAGGGCGGCA TAGTCCTGGT GCGCAATATT GCGCAGCTA GCTGCTCTTA	2100
GCTTCGGTGA CCGTGGTTAA TTATGACCTC CTTACCA	2138

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 460 amino acids

(B) TYPE: amino acid

174

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

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Met Thr Gln Ser Gln Thr Val Thr Val Asp Gln Gln Glu Ile Leu Asn
 1           5           10           15

Arg Ala Asn Glu Val Glu Ala Pro Met Ala Asp Pro Pro Thr Asp Val
 20           25           30

Pro Ile Thr Pro Cys Glu Leu Thr Ala Ala Lys Asn Ala Ala Gln Gln
 35           40           45

Leu Val Leu Ser Ala Asp Asn Met Arg Glu Tyr Leu Ala Ala Gly Ala
 50           55           60

Lys Glu Arg Gln Arg Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Ala
 65           70           75           80

Tyr Gly Glu Val Asp Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly
 85           90           95

Glu Gly Thr Val Gln Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser
100           105           110

Ser Ala Glu Leu Thr Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro
115           120           125

Asn Phe Met Asp Leu Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp
130           135           140

Gln Gly Ala Ser Leu Ala His Phe Ala Asp Gly Trp Asn Thr Phe Asn
145           150           155           160

Leu Thr Leu Gln Gly Asp Val Lys Arg Phe Arg Gly Phe Asp Asn Trp
165           170           175

Glu Gly Asp Ala Ala Thr Ala Cys Glu Ala Ser Leu Asp Gln Gln Arg
180           185           190

Gln Trp Ile Leu His Met Ala Lys Leu Ser Ala Ala Met Ala Lys Gln
195           200           205

Ala Gln Tyr Val Ala Gln Leu His Val Trp Ala Arg Arg Glu His Pro
210           215           220

Thr Tyr Glu Asp Ile Val Gly Leu Glu Arg Leu Tyr Ala Glu Asn Pro
225           230           235           240

Ser Ala Arg Asp Gln Ile Leu Pro Val Tyr Ala Glu Tyr Gln Gln Arg
245           250           255

Ser Glu Lys Val Leu Thr Glu Tyr Asp Asn Lys Ala Ala Leu Glu Pro
260           265           270

```

175

Val Asn Pro Pro Lys Pro Pro Pro Ala Ile Lys Ile Asp Pro Pro Pro
 275 280 285
 Pro Pro Gln Glu Gln Gly Leu Ile Pro Gly Phe Leu Met Pro Pro Ser
 290 295 300
 Asp Gly Ser Gly Val Thr Pro Gly Thr Gly Met Pro Ala Ala Pro Met
 305 310 315 320
 Val Pro Pro Thr Gly Ser Pro Gly Gly Gly Leu Pro Ala Asp Thr Ala
 325 330 335
 Ala Gln Leu Thr Ser Ala Gly Arg Glu Ala Ala Ala Leu Ser Gly Asp
 340 345 350
 Val Ala Val Lys Ala Ala Ser Leu Gly Gly Gly Gly Gly Gly Val
 355 360 365
 Pro Ser Ala Pro Leu Gly Ser Ala Ile Gly Gly Ala Glu Ser Val Arg
 370 375 380
 Pro Ala Gly Ala Gly Asp Ile Ala Gly Leu Gly Gln Gly Arg Ala Gly
 385 390 395 400
 Gly Gly Ala Ala Leu Gly Gly Gly Gly Met Gly Met Pro Met Gly Ala
 405 410 415
 Ala His Gln Gly Gln Gly Gly Ala Lys Ser Lys Gly Ser Gln Gln Glu
 420 425 430
 Asp Glu Ala Leu Tyr Thr Glu Asp Arg Ala Trp Thr Glu Ala Val Ile
 435 440 445
 Gly Asn Arg Arg Arg Gln Asp Ser Lys Glu Ser Lys
 450 455 460

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 377 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Ala Gly Asn Val Thr Ser Ala Ser Gly Pro His Arg Phe Gly Ala Pro
 1 5 10 15
 Asp Arg Gly Ser Gln Arg Arg Arg Arg His Pro Ala Ala Ser Thr Ala
 20 25 30
 Thr Glu Arg Cys Arg Phe Asp Arg His Val Ala Arg Gln Arg Cys Gly
 35 40 45

Phe Pro Pro Ser Arg Arg Gln Leu Arg Arg Arg Val Ser Arg Glu Ala
 50 55 60
 Thr Thr Arg Arg Ser Gly Arg Arg Asn His Arg Cys Gly Trp His Pro
 65 70 75 80
 Gly Thr Gly Ser His Thr Gly Ala Val Arg Arg Arg His Gln Glu Ala
 85 90 95
 Arg Asp Gln Ser Leu Leu Leu Arg Arg Arg Gly Arg Val Asp Leu Asp
 100 105 110
 Gly Gly Gly Arg Leu Arg Arg Val Tyr Arg Phe Gln Gly Cys Leu Val
 115 120 125
 Val Val Phe Gly Gln His Leu Leu Arg Pro Leu Leu Ile Leu Arg Val
 130 135 140
 His Arg Glu Asn Leu Val Ala Gly Arg Arg Val Phe Arg Val Lys Pro
 145 150 155 160
 Phe Glu Pro Asp Tyr Val Phe Ile Ser Arg Met Phe Pro Pro Ser Pro
 165 170 175
 His Val Gln Leu Arg Asp Ile Leu Ser Leu Leu Gly His Arg Ser Ala
 180 185 190
 Gln Phe Gly His Val Glu Tyr Pro Leu Pro Leu Leu Ile Glu Arg Ser
 195 200 205
 Leu Ala Ser Gly Ser Arg Ile Ala Phe Pro Val Val Lys Pro Pro Glu
 210 215 220
 Pro Leu Asp Val Ala Leu Gln Arg Gln Val Glu Ser Val Pro Pro Ile
 225 230 235 240
 Arg Lys Val Arg Glu Arg Cys Ala Leu Val Ala Arg Phe Glu Leu Pro
 245 250 255
 Cys Arg Phe Phe Glu Ile His Glu Val Gly Phe Thr Gly Arg Gly His
 260 265 270
 Pro Arg Arg Ile Gly
 275

(2) INFORMATION FOR SEQ ID NO:186:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:186:

177

Arg Val Ala Ala Ser Phe Ile Asp Trp Leu Asp Ser Pro Asp Ser Pro
 1 5 10 15
 Leu Asp Pro Ser Leu Val Ser Ser Leu Leu Asn Ala Val Ser Cys Gly
 20 25 30
 Ala Glu Ser Ser Ala Ser Ser Ser Ala Arg Ser Gly Asn Gly Ser Arg
 35 40 45
 Trp Thr Ser Met Pro Ser Gly Thr Arg Pro Gly Pro Arg Arg Ala Thr
 50 55 60
 Ser Arg Asp Asp Arg Arg Ser Ala Thr Ser Val Ile Pro Ser Arg Arg
 65 70 75 80
 Ser Val Ala Pro Arg Ala Glu Phe Gly Thr Arg Leu Ala Ser His Arg
 85 90 95
 Ala Ser Pro Ser Asn Ala Cys Pro Val Arg Ile Val Thr Ser Ala Ser
 100 105 110
 Gly Arg Pro Ile Ser Ser Pro Pro Ile Val Arg Ser Arg Ser Cys Val
 115 120 125
 Asp Lys Asn Gly Arg Arg Cys Ala Ser Gly Tyr Arg Arg Leu Asn Arg
 130 135 140
 Ala Arg Ser Ser Ser Ile Ala Ala Arg Cys Arg Thr Ile Gly Thr Phe
 145 150 155 160
 Arg Arg Ser Arg Tyr Ser Ala Ser Met Arg Val Ser Thr Asn Ser Pro
 165 170 175
 His Val Thr His Gly Val Ala Pro Gly Val Thr Arg Arg Ile Gly Gly
 180 185 190

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 196 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Gln Glu Arg Pro Gln Met Cys Gln Arg Val Ser Glu Ile Glu Pro Arg
 1 5 10 15
 Thr Gln Phe Phe Asn Arg Cys Ala Leu Pro His Tyr Trp His Phe Pro
 20 25 30
 Ala Val Ala Val Phe Ser Lys His Ala Ser Leu Asp Glu Leu Ala Pro

with

35		40		45
Arg	Asn	Pro	Arg	Arg
50			Ser	Ser
			Arg	Arg
			Asp	Ala
			Glu	Asp
			Arg	Arg
			Val	
				60
Ile	Phe	Ala	Ala	Thr
65			Leu	Val
			Ala	Val
			Asp	Pro
			Pro	Leu
			Arg	Gly
				Ala
				80
Gly	Gly	Glu	Ala	Asp
			Gln	Leu
			Ile	Asp
			Leu	Gly
			Val	Cys
			Arg	Arg
			Gln	
				95
Ala	Gly	Arg	Val	Arg
			Arg	Arg
			Gly	Gln
			Glu	Leu
			His	His
			Arg	His
			Arg	His
				110
Gln	Gly	Ala	Ala	Pro
			Asp	Leu
			Arg	Arg
			Arg	Arg
			Arg	Arg
			His	Arg
			Arg	Val
				125
Gln	Gln	His	Arg	Arg
			Leu	Gln
			Arg	Val
			Arg	Gln
			Leu	Arg
			Arg	Tyr
			Val	
				140
Gln	Thr	Ala	His	His
			Arg	Arg
			Phe	Ala
			Arg	Thr
			Asp	Arg
			Val	Arg
			His	
				160
His	Val	Arg	Gly	Pro
			Ser	Asn
			His	Arg
			Arg	Arg
			Arg	Arg
			Val	Tyr
			Arg	Gly
				175
Arg	His	Ser	Gly	Ala
			Gly	Gly
			Cys	Pro
			Ala	Gly
			Gly	Ala
			Gly	Ser
			Val	
				190
Gly	Gly	Ser	Ala	
				195

(2) INFORMATION FOR SEQ ID NO. 192:

(2) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO: 188.

```

Val Arg Cys Gly Thr Leu Val Pro Val Pro Met Val Glu Phe Leu Thr
1      5      10
Ser Thr Asn Ala Pro Ser Leu Pro Ser Ala Tyr Ala Glu Val Asp Lys
20      25      30
Leu Ile Gly Leu Pro Ala Gly Thr Ala Lys Arg Trp Ile Asn Gly Tyr
35      40      45
Glu Arg Gly Gly Lys Asp His Pro Pro Ile Leu Arg Val Thr Pro Gly
50      55      60
Ala Thr Pro Trp Val Thr Trp Gly Glu Phe Val Glu Thr Arg Met Leu

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179

68	70	75	80
Ala Glu Tyr Arg Asp Arg Arg Lys Val Pro Ile Val Arg Glu Arg Ala	85	90	95
Ala Ile Glu Glu Leu Arg Ala Arg Phe Asn Leu Arg Tyr Pro Leu Ala	100	105	110
His Leu Arg Pro Phe Leu Ser Thr His Glu Arg Asp Leu Thr Met Gly	115	120	125
Gly Glu Glu Ile Gly Leu Pro Asp Ala Glu Val Thr Ile Arg Thr Gly	130	135	140
Gln Ala Leu Leu Gly Asp Ala Arg Trp Leu Ala Ser Leu Val Pro Asn	145	150	155
Ser Ala Arg Gly Ala Thr Leu Arg Arg Leu Gly Ile Thr Asp Val Ala	165	170	175
Asp Leu Arg Ser Ser Arg Glu Val Ala Arg Arg Gly Pro Gly Arg Val	180	185	190
Pro Asp Gly Ile Asp Val His Leu Leu Pro Phe Pro Asp Leu Ala Asp	195	200	205
Asp Asp Ala Asp Asp Ser Ala Pro His Glu Thr Ala Phe Lys Arg Leu	210	215	220
Leu Thr Asn Asp Gly Ser Asn Gly Glu Ser Gly Glu Ser Ser Gln Ser	225	230	235
Ile Asn Asp Ala Ala Thr Arg Tyr Met Thr Asp Glu Tyr Arg Gln Phe	245	250	255
Pro Thr Arg Asn Gly Ala Gln Arg Ala Leu His Arg Val Val Thr Leu	260	265	270
Leu Ala Ala Gly Arg Pro Val Leu Thr His Cys Phe Ala Gly Lys Asp	275	280	285
Arg Thr Gly Phe Val Val Ala Leu Val Leu Glu Ala Val Gly Leu Asp	290	295	300
Arg Asp Val Ile Val Ala Asp	305	310	

(2) INFORMATION FOR SEQ ID NO:189:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3073 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

CTCCTGCCCCA TTCCGCACGA GCTGAGCAGC CCAAGGGGCC GTTCGGCGAA GTCATCGAGG	60
CATTGCCCCA CCGGCTGGCC GGCAGGGTA AGCAAATCAA CACCAAGCTG AACAGCTGT	120
CCAGAGGCTT GAACGCTTG AATGAGGGCC GCGGCGACTT CTTCGGCTG GTACCGAGCC	180
TGGCGCTATT CGTCAACGCG CTACATCAGG AGGACCAACA GTTCGTGCGG TTGAACAAGA	240
ACCTTGCGGA GTTCACCGAC AGGTTGACCC ACTCGGATGC GGCCTGTGCG AACGCCATCC	300
AGCAATTGCA CAGCTTGCTC GCGTCCGCG GCGGTTCTT CCGCAAGAAC CGCGAGGTGC	360
TGACCGATGA CTTCAATAAT CTCGCGACCG TGACCACCAC GTTGCTGCGG CCGGATCCGT	420
TGGATGGGTT GGAGACGCTC CTGCACATCT TCCGAGGCT GCGGCGAAC ATTAACCAGC	480
TTTACCATCC GACACACGCT GCGTGGTGT CCGTTTCCCG GTTCACGAAT TTGCGCAACC	540
CGATGGAGTT CATCTGCAGC TCGATTCAGG CCGGTAGCG GCTCGGTTAT CAAGAGTCGG	600
CCGAAGTCTG TCGCGAGTAT CTGGCGCCAG TCGTCGATGC GATCAAGTTC AACTACTTTC	660
CGTTGCGCTT GAAGGTGGCC AGCAGCGCTT CGCACTGCG TAAAGAGATC GCGTACTCCG	720
AGCGCGGCTT GCAGCGCGCC AACGGGTACA AGGACACGAC GGTGCGCGGC ATCTGGGTGC	780
CGGATACGCC GTTGTACAC CCGAACACGC AGCGCGGTTG GGTGGTGGCA CCGGGGATGC	840
AAGGGGTTCA GGTGGGACCG ATCAGCGAGG GTTCTCTGAC GCGGAGTCC CTGGCGGAAC	900
TGATGGGTGG TCCGATATC GCGGCTCGCT GTTCAGGCTT GCAAAGCTCG CCGGAGCCCC	960
CGAATGCGTA CGACGAGTAC CCGTGTCTGC CCGGATCGG TTTACAGGCC CCGAGGTGC	1020
CGATACCAGC GCGGCTCTCT GCGGCGGACG TAATCCCGGG TCGGCTGGCA CCGGTCTTGG	1080
CGGCGATCTT GTTCCGAGA GATCGCCCG CAGCGTGGGA AAAGTTGAG TACATGGGCC	1140
TCTTGTCTCT GTGCGCGCG CTGGCGACCT TCGTCTCGG GGTGTGATCT AGCCCCCGCC	1200
GTGGAACGAT GCGGATCGG CAGCTGTTGA TACCGGCGAT CAGCGGCTTG GCGTGGATCG	1260
CGGCATTCTT CCGACATTCT TGGTACCGCA CAGAAGATCC GGTGATAGAC ATGCGCTTGT	1320
TCCAGAACCG AGCGGTGCG CAGGCCAACA TGAGGATGAC GGTGCTCTCC CTGCGGCTGT	1380
TTGGCTGCTT GTTCTCTCT CCGAGCTACC TCCAGCAAG GTTGACCAA TCAGGATGC	1440
AATGCGGGGT GCATATCATC CCGAGGGCC TCGGTCCAT GCTGCGGATG CCGATCGGCC	1500
GAGCGATGAT GGACCGACCG GGACCGGCGA AGATCTGCT GTTGGGATC ATGCTGATCG	1560
CTGCGGCTT GCGCACCTTC GCGTTTGGTG TCGCGCGCA AGCGGACTAC TTACCGATTC	1620

TGCGGACCGG GCTGGCAATC ATGGGCATGG GCATGGGCTG CTCCATGATG CCACTGTCCG	1680
GGGCGGCACT GCAGACCTTG GCGGCACATC AGATCGCTCG CGGTTGACG CTGATCAGCG	1740
TCAACCAGCA GGTGGGCGGT TCGATAGGGA CGGCACTGAT GTGGGTGCTG CTERCCTACC	1800
AGTTCAATCA CAGCGAAATC ATCGCTACTG CAAAGAAAGT CGCACTGACC CCAGAGAGTG	1860
GCGCGGGGCG GGGGCGGCGG GTTGACCTTT CCTGGCTACC GCGCCAAACC AACTTCGGCG	1920
CGCACTGCTT GCATGACCTT TCGACGGCTT ACCGGGTGGT ATTCTGATA GCGACCGCGC	1980
TAGTGGTCTC GACGCTGATC CCGCGGGCAT TCTGCCGAA ACAGCAGGCT AGTCATCGAA	2040
GAGCACCTTT GCTATCCGCA TGACGTCTGC TT	2072

(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1923 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TCACCCCGGA GAAGTCCTTC GTGACGACC TGGACATCGA CTCGCTGTCC ATGGTCGAGA	60
TGCGCTGCA GACCGAGGAC AACTACGCG TCAAGATCCC CGACGAGGAC CTCGCCCTTC	120
TGCGTACCTT CGGTGACCTT GTGGCTTACA TCGAGAAGCT CGAGGAAGAA AACCCTGAGG	180
CGGCTCAGGC GTTGGCGGCG AAGATTGAGT CGGAGAAGCC CGATGCGGCA CGAGCAGATC	240
GGTGCGTTTC ACCGACATCG CAAGCTCGAG ACCCGCGTCC TCTCTTTGCA CGCTCAGCCA	300
GGTGGGCTG TCGCGGCTT CCAGCAAGTG TCGGACCCAC ACCAAGGGAC CCTGCGGAAA	360
GCTGACTGAT CCGCGGACCA CATAGTGGAT GCGACCGTGG CTGACAATTG CGCCGGGTCC	420
GAGTTGGCGG GGGCGGAATT GCGGCATTGC GTGGAAGGCC AGCGGATCCC GCGGCGGCGC	480
CGCGTGGCTT GTGTCTTTTG GCGCGCGGAT GCGCAGAGG AGAAGGACGA TGGCGGGCAT	540
GAACAGCGCC ACCGCAATCA CGACGAGCAG ATTTCCACCG CATACCTCTT CGTACCGCTG	600
CGCGCGGCTT GGTGATCGG TCGCATATCG ATGGCGCGGT TTAACGTAAC AGCTTTCCCG	660
GGACCGGGG TCACACCGG CGAGTTGTCC GCGCGGGAAC CGGCAAGTC TCGGCGGCGG	720
TCACCGCAGC TCACTGGTGC ACCATCCGGG TGTGGGTGAG CGTGCAACTC AAACACACTC	780
AACGCGAAGG GTTGTCTAGG TCACGAGTC AACCTCGACC CGCAATCGCT CGTACGTTTC	840

GACCCGCGGC AGGTGCGGAG TCAGCAGCTT TCGCCCGGCA GCTTTGCGCG TGAAGCCGAC 900
 CAGCGCATCG TAGGTTGCGC CACCGGTGAC ATCTGTCTCG GCGAGGTGGT CCGTCAAGCC 960
 CCGATATGAG CAGGCTATCA GTGCCAGGTA GTTGCTGAG GTGATGTCCG CCAAGTAGGC 1020
 GTGACCGGCA ACAGGCGCAA TACGATGCGG CCGTGGTAGC CCGGTCAAGA CCGAATAGGT 1080
 TTCCACAGGC GCGTSCGCGA TCAGATGGAC GCCACGGTTG AGCGCGCGCA CCGCGGCTTC 1140
 GTGCCCTTCG TGCCAGGTCT CGAATCCGCG AACCAGCAGC CTGGTGTCTG GTCCGATCAC 1200
 CGCGTGTGTC GATCGAGCGT TTCCCGAAGC ATTTCTCTCG TCAACGGGGG CAGCGGACGT 1260
 TGTGCGCGTC CGACGAGAAC CGAGCCTTCC CGAAGAGTT CGACACCGGT CCGGCGCGGC 1320
 TCAATCTCGA TGCGCCCATC GCGCTCGGTG ATCTCCACTT GGTGTTCCG GCGCAGGCA 1380
 AGCGGCTGCG GAATCGCGTT GCGAATCACC AGACCTCTCG CGACATCGAT GGTGTGTCGC 1440
 ATGCTAGGAA ATTTACCATC GCACGTTCCA TAGCGGTGTC CTGCGCGGGA TGTGCGGACG 1500
 ATCCGCTAGC GTATCGAAGC ATTGTTTCGG AAATGGCTGA GGGAGCGTGC GGTGCGGTCG 1560
 ATGGGTGTCG ATCCGCGTT GACCCGATGC GCGCTGTGCG TCATCGAGAG TGGGCGTGGT 1620
 CCGCAGCTCA CCGCGCTGGA TGTGAGCGTG GTGCGCACAC CTTCGGATGC GGCCTTGCGG 1680
 CAGCGCCTGT TGCCATCAG CGATGCGGTC GAGCACTGCG TCGACACCCA TCATCCGAG 1740
 GTGTGGCTA TCGAACGGT GTTCTCTCAG CTCACGTGA CCGCGTGAT GGGCACCGCC 1800
 CAGCGCGCGG GGTGATGCG CTGCGCGCGG GCCAAGCTG GTGTGACGT GCATTTCCAT 1860
 ACCCGCAGCG AGTCAAGGC GCGGTCACCT GGCACCGGT CCGCAGACAA GGTCTAGGTC 1920
 ACC 1923

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1055 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:191:

CTGGCGTGGC AGTGTACCG CCGATATGAG GTCCGCATTC AATTTCGCG CCCCCCGGA 50
 CCGTTCGCA CCGAATCTCG ACCACCGGT CCGTCAATTG CCGAAGGTG CCAAGTGGT 120
 GCGCAATGTG GTGCTGGGTT TCTTGAACGA AGGCTTGCGG TATCGGGTGC CCTACCCCA 180
 AACRACGCA GTCCAGGAT CCGGTGCGCG GCGGCGGATT CCGAGCGCA TGTGCTAGCC 240

GGGGATGGTT CAGACCTAAC GGTTCGCTAG GTGAAAACCC GCGCCAGGGC CGCTGGACCG 300
 GGTTCATGCCA GCGAAATTAG AAAACCCGGG ATATTGTCCG CGGATTGTCA TACGATGCTG 360
 AGTGCTTGCT GGTTCGTGTT TACCCATTGA GTGTGGATGT GTTGAGACCC TGGCCTGGAA 420
 GGGGACAACG TGCTTTTGCC TCTTGGTCCG CTTTTCGCGC CCGACCCCGT GGTGCGAAAA 480
 CCGGCTGAGT CCGGATGCT CCGCGGTTG TCGTTTCCGC TCAGCTGGGG AGTGCTGTG 540
 CCACCCGATG ATTATGACCA CTGGCCGCTT GCGCGGAGG ACAGCGCCGA TGTGATGTC 600
 CAGGCGCCCG AAGGGGCGGA CGCAGAGCCC GCGGCCATGG ACCAGTGGGA TGAGTGGCAG 660
 GCGTGGAAAG AGTGGGTGGC GGAGAACGCT GAACCCGCTT TTGAGGTGCC ACCGAGTAGC 720
 AGCAGCTGA TTCCGATTC TCCGCGGCC GGTAGGAGA GGGGCGCCAG ACTGTCTTA 780
 TTGACCACT GATCGCCGT CTCGTGTTC CCGCGCGCGG CTATGACAAC AGTCAATGTG 840
 CATGACAAT TACAGTATT AGTCCAGGT TCAACAAGGA GACAGGCAAC ATGGCAACAC 900
 GTTTCATGAC GGATCCGCAC CGCATGCCG ACATGCGCGG CCGTTTGGAG GTGCACGCCC 960
 AGACGCTGGA GGACGAGCT CCGCGGATGT GCGCTTCCG GCAAAACATC TCGGCGCCGG 1020
 CCTGGAGTGG CATGCCCAG GCGACTTGGC TAGAC 1088

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 159 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

CCGCTTCGTT GTTGGCATA TCCGCGCGG CCGCTTCGAC CGCACTGGCC GTGCGTGTG 60
 TCCGGCTGA CCACCGGAT CCGCGAACCA TCCGAGTCA CCGCGCAATG ATCCACCTCG 120
 CCGAGCTGCT CACCCAGCCA CCGGCGGTTG TCCGACAGG CCGCATCAC CTGCGTATAG 180
 CCGTCCGCCC CCGCGCCAG GAGTGTGTAG TACTGCCCCA CCACCTGTT ACCGGGAGGG 240
 GAGAAATTCA GGTGAAGGT CCGCATGTG CCGCGGAGT AGTTGACCCG GAAAACCGA 300
 TCTCCGSCA GTGCTCGGG CCGCGCCAC ACCACAAAC CCGCGCCGG ATAGTTCAG 360

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 380 base pairs

184

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

```

AACGGGCCCC TGGGACCCGC TCCTCTAAGG GCTCTCGTTG GTCCCATGAA GTGCTGGAAG      60
GATGCATCTT GGCAGATTCC CCGAGAGACA AAACAGCCGC TAGTCCTAGT CCGAGTCGCC      120
CGCAAAGTTC CTCGAATAAC TCGTACCCCG GAGCGCCAAA CCGGCTCTCC TTCGCTAAGC      180
TCCCGCAACC ACTTGAGGTT CCGGAGCTCC TTGACCTCCA GACCGATTCC TTCGAGTGGC      240
TGATCGGTTT GCGGCGCTCG CCGGAATCCC CCGCCGAGCG GGGTATGTC AACCCAGTGG      300
GTGGCCTCGA AGAGGTCTTC TACGAGCTGT CTCGATCGA GGACTTCTCC      360
  
```

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 679 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

```

Glu Gln Pro Lys Gly Pro Phe Gly Glu Val Ile Glu Ala Phe Ala Asp      1
1           5           10           15
Gly Leu Ala Gly Lys Gly Lys Glu Ile Asn Thr Thr Leu Asn Ser Leu      20
20          25          30
Ser Gln Ala Leu Asn Ala Leu Asn Glu Gly Arg Gly Asp Phe Phe Ala      35
35          40          45
Val Val Arg Ser Leu Ala Leu Phe Val Asn Ala Leu His Gln Asp Asp      50
50          55          60
Gln Gln Phe Val Ala Leu Asn Lys Asn Leu Ala Glu Phe Thr Asp Arg      65
65          70          75          80
Leu Thr His Ser Asp Ala Asp Leu Ser Asn Ala Ile Gln Gln Phe Asp      85
85          90          95
Ser Leu Leu Ala Val Ala Arg Pro Phe Phe Ala Lys Asn Arg Glu Val      100
100         105         110
Leu Thr His Asp Val Asn Asn Leu Ala Thr Val Thr Thr Thr Leu Leu      115
115         120         125
Gln Pro Asp Pro Leu Asp Gly Leu Glu Thr Val Leu His Ile Phe Pro      130
130         135         140
  
```


185

Thr Leu Ala Ala Asn Ile Asn Gln Leu Tyr His Pro Thr His Gly Gly
 145 150 155 160
 Val Val Ser Leu Ser Ala Phe Thr Asn Phe Ala Asn Pro Met Glu Phe
 165 170 175
 Ile Cys Ser Ser Ile Gln Ala Gly Ser Arg Leu Gly Tyr Gln Glu Ser
 180 185 190
 Ala Glu Leu Cys Ala Gln Tyr Leu Ala Pro Val Leu Asp Ala Ile Lys
 195 200 205
 Phe Asn Tyr Phe Pro Phe Gly Leu Asn Val Ala Ser Thr Ala Ser Thr
 210 215 220
 Leu Pro Lys Glu Ile Ala Tyr Ser Glu Pro Arg Leu Glu Pro Pro Asn
 225 230 235 240
 Gly Tyr Lys Asp Thr Thr Val Pro Gly Ile Trp Val Pro Asp Thr Pro
 245 250 255
 Leu Ser His Arg Asn Thr Gln Pro Gly Trp Val Val Ala Pro Gly Met
 260 265 270
 Gln Gly Val Gln Val Gly Pro Ile Thr Gln Gly Leu Leu Thr Pro Glu
 275 280 285
 Ser Leu Ala Glu Leu Met Gly Gly Pro Asp Ile Ala Pro Pro Ser Ser
 290 295 300
 Gly Leu Gln Thr Pro Pro Gly Pro Pro Asn Ala Tyr Asp Glu Tyr Pro
 305 310 315 320
 Val Leu Pro Pro Ile Gly Leu Gln Ala Pro Gln Val Pro Ile Pro Pro
 325 330 335
 Pro Pro Pro Gly Pro Asp Val Ile Pro Gly Pro Val Pro Pro Val Leu
 340 345 350
 Ala Ala Ile Val Phe Pro Arg Asp Arg Pro Ala Ala Ser Glu Asn Phe
 355 360 365
 Asp Tyr Met Gly Leu Leu Leu Leu Ser Pro Gly Leu Ala Thr Phe Leu
 370 375 380
 Phe Gly Val Ser Ser Ser Pro Ala Arg Gly Thr Met Ala Asp Arg His
 385 390 395 400
 Val Leu Ile Pro Ala Ile Thr Gly Leu Ala Leu Ile Ala Ala Phe Val
 405 410 415
 Ala His Ser Trp Tyr Arg Thr Glu His Pro Leu Ile Asp Met Arg Leu
 420 425 430
 Phe Gln Asn Arg Ala Val Ala Gln Ala Asn Met Thr Met Thr Val Leu

185

435	440	445
Ser Leu Gly Leu Phe Gly Ser Phe Leu Leu Leu Pro Ser Tyr Leu Gln 450	455	460
Gln Val Leu His Gln Ser Pro Met Gln Ser Gly Val His Ile Ile Pro 465	470	475
Gln Gly Leu Gly Ala Met Leu Ala Met Pro Ile Ala Gly Ala Met Met 485	490	495
Asp Arg Arg Gly Pro Ala Lys Ile Val Leu Val Gly Ile Met Leu Ile 500	505	510
Ala Ala Gly Leu Gly Thr Phe Ala Phe Gly Val Ala Arg Gln Ala Asp 515	520	525
Tyr Leu Pro Ile Leu Pro Thr Gly Leu Ala Ile Met Gly Met Gly Met 530	535	540
Gly Cys Ser Met Met Pro Leu Ser Gly Ala Ala Val Gln Thr Leu Ala 545	550	555
Pro His Gln Ile Ala Arg Gly Ser Thr Leu Ile Ser Val Asn Gln Gln 565	570	575
Val Gly Gly Ser Ile Gly Thr Ala Leu Met Ser Val Leu Leu Thr Tyr 580	585	590
Gln Phe Asn His Ser Glu Ile Ile Ala Thr Ala Lys Lys Val Ala Leu 595	600	605
Thr Pro Glu Ser Gly Ala Gly Arg Gly Ala Ala Val Asp Pro Ser Ser 610	615	620
Leu Pro Arg Gln Thr Asn Phe Ala Ala Gln Leu Leu His Asp Leu Ser 625	630	635
His Ala Tyr Ala Val Val Phe Val Ile Ala Thr Ala Leu Val Val Ser 645	650	655
Thr Leu Ile Pro Ala Ala Phe Leu Pro Lys Gln Gln Ala Ser His Arg 660	665	670
Arg Ala Pro Leu Leu Ser Ala 675		

(2) INFORMATION FOR SSS ID NO. 1486.

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Thr Pro Glu Lys Ser Phe Val Asp Asp Leu Asp Ile Asp Ser Leu Ser
 1 5 10 15
 Met Val Glu Ile Ala Val Gln Thr Glu Asp Lys Tyr Gly Val Lys Ile
 20 25 30
 Pro Asp Glu Asp Leu Ala Gly Leu Arg Thr Val Gly Asp Val Val Ala
 35 40 45
 Tyr Ile Gln Lys Leu Glu Glu Glu Asn Pro Glu Ala Ala Gln Ala Leu
 50 55 60
 Arg Ala Lys Ile Glu Ser Glu Asn Pro Asp Ala Ala Arg Ala Asp Arg
 65 70 75 80
 Cys Val Ser Pro Thr Ser Glu Ala Arg Asp Ala Arg Arg Pro Leu Ala
 85 90 95
 Arg Ser Ala Arg Leu Ala Cys Arg Arg Leu Pro Ala Ser Val Pro Thr
 100 105 110
 Thr Arg Arg Asp Pro Arg Glu Arg
 115 120

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Leu Ala Cys Glu Cys His Arg Arg Tyr Asp Val Gly Ile Gln Phe Arg
 1 5 10 15
 Gly Pro Ala Gly Pro Val Ala Thr Gln Ser Gly Pro Pro Gly Pro Ser
 20 25 30
 Ile Ala Glu Gly Arg Gln Val Arg Ala Gln Cys Gly Ala Gly Phe Leu
 35 40 45
 Glu Arg Arg Pro Ala Val Ser Gly Ala Leu Pro Pro Asn Asn Ala Ser
 50 55 60
 Pro Gly Ile Arg Ser Arg Ala Ala Asp Ser Gln Arg His Leu Leu Ala
 65 70 75 80
 Gly Asp Gly Ser Asp Val Thr Val Gly
 85

(2) INFORMATION FOR SEQ ID NO:197:

188

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Ala Ser Leu Leu Ala Tyr Ser Ala Ala Ala Ser Thr Ala Leu Ala
 1 5 10 15

Val Ala Cys Val Arg Ala Asp His Arg Asp Arg Arg Thr Ile Arg Asp
 20 25 30

His Leu Ala Met Ile His Leu Ala Gln Leu Val Thr Gln Pro Pro Gly
 35 40 45

Gly Val Arg Gln Arg Leu His His Leu Gly Ile Ala Val Ala Pro Gln
 50 55 60

Pro Gln Glu Val Val Val Leu Ala His His Leu Val Thr Gly Thr Gly
 65 70 75 80

Glu Val Gln Gly Glu Gly Arg His Val Ala Ala Glu Val Val Asp Pro
 85 90 95

Glu Asn Gln Ile Leu Arg Gln Val Leu Gly Pro Ala Pro His Asp Lys
 100 105 110

Pro Asp Ala Gly Ile Gly Gln
 115

(2) INFORMATION FOR SEQ ID NO:198:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Arg Ala Arg Gly His Arg Ser Ser Lys Gly Ser Arg Trp Ser His Glu
 1 5 10 15

Val Leu Glu Gly Cys Ile Leu Ala Asp Ser Arg Gln Ser Lys Thr Ala
 20 25 30

Ala Ser Pro Ser Pro Ser Arg Pro Gln Ser Ser Ser Asn Asn Ser Val
 35 40 45

Pro Gly Ala Pro Asn Arg Val Ser Phe Ala Lys Leu Arg Glu Pro Leu
 50 55 60

189

Glu Val Pro Gly Leu Leu Asp Val Gln Thr Asp Ser Phe Glu Trp Leu
 65 70 75 80
 Ile Gly Ser Pro Arg Trp Arg Glu Ser Ala Ala Glu Arg Gly Asp Val
 85 90 95
 Asn Pro Val Gly Gly Leu Glu Glu Val Leu Tyr Glu Leu Ser Pro Ile
 100 105 110
 Glu Asp Phe Ser
 115

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

TGCTACGCGAG CAATCGCTTT GTGACAGAT GTGGATGCCG GCGTCGCTGC TGGCGATGGC 60
 GTGAAAGCGG CGACGTGTT CCGCGCATTC GGGGAGAACA TCGAACTGCT CAAAGGCGTG 120
 GTGCGGGGCG CCATCGATCG GTTCGCGGAC GAGCGGACCT GCACGCACTG TCAACACCAC 180
 GCGCGTGTTT CTTGCGGTT CAGCTGCCA TGAGGTGCT GCTGACCGGC GCGGCGCGCT 240
 TCATCGGTC GCGGTGGAT GCGCGTTAC GGGCTCGGG TCACGACGTG GTGGGCGTGG 300
 ACCCGCTGCT GCGCGCGCG CACGGGCCAA ACCCGTCTT GCGACCGGCG TCGCAGCGGG 360
 TCGACGTGCG CGACGCCAGC GCGCTGGCCC CTTGTTGGC CGGTGTGAT CTGTTGTGTC 420
 ACCAGCGCGC CATGTTGGT GCGGCGTCA ACCCGCGGA CGCAGCGCG TATGCGGCGC 480
 ACAACGATT CCGCACACG GTGCTGCTG CCGAGATGTT CCGCGCGCG GTCGCGCGTT 540
 TGGTCTGCG GTGCTCATG GTGGTTTAC GCGAGGGGCG CTATGACTGT CCGCAGCATG 600
 GACCGGTGGA CCGGCTGCG CGCGCGCGAG CCGACCTGGA CAATCGGCTC TTCGAGCACC 660
 GTTCCCGCG GTCGCGCGAG CCAATCATCT GCGAATTGGT CGACGAAGAT GCGCGGTTGC 720
 GCGCGCGCG CTTGTACCG GCAGCAAGAC CCGCGAGGAG CACTACGCG TCGCTGCTGC 780
 GGAACGGAAT GCGGTTGCG TGGTGGCGTT 811

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

GTCCCCGCGAT GTGGCCGAGC ATGACTTTCC GCAACACCGG CGTAGTAGTC GAAGATATCG	60
GACTTTCTGG TCCCGGTGGC GGGATAGAGC ACGTGTGGC GTTGGTCAGC CTCACCCGTT	120
GCTCGGACGC CGAACCCATG CTTTCAACCT AGCTGTCCG TCACACAAGT CGCGAGCGTA	180
ACCTCACGCT CAAATATCGC GTGGAAATTC GCCGTGACCT TCCGCTGGCG GACAAATCAAG	240
GCATACTCAC TTACATCGCA GCCATTTGGA CGGTTTGGAT CCGCTTCGGG CTGGTGAACG	300
TGCGSSTCAA GGTGTACAGC GCTACCGCAG ACCACGACAT CAGTTTCCAC CAGGTGCAGC	360
CGAAGGACAA CGGACCGATC CGGTACAAGC GCGTCTCGCA GCGGTGTGGC GAGGTGGTCG	420
ACTACCGCGA TCTTGCCCGG GCTTACGAGT CCGCGGACCG CGAATGGTG GCGATCAGCG	480
ACGACGACAT CGCCAGCTTG CCTGAAGAAC GCAGCCCGGA GATCGAGGTC TTGGAGTTCC	540
TGCGCGCCGC CGACGTGGAC CGGATGATGT TCGACCGCAG CTACTTTTTG GAGGCTGATT	600
CGAAGTCGTC GAAATCTAT GTCTCTCTCG CTAAAGACCT CGCCGAGACC GAGCGSATCG	660
CGATCGTGA TCGCCCGACC GCGCGTGAAT GCAGGAAAAA TAAGAGCCGC TATCCACAAT	720
TGCGCGTCGA GCTCGGCTAC CACAAAGGCT AGAAGCATCG AGACATTCCC GAGGTGAAGT	780
GCGGCTCTAT AGAAGCGGCT CTGCGGCTTT ATCAAAGCGA AAATACGCTT ACTCATGCCA	840
TGCGCGCGTC TCACCGGATG CGACGTTTTT GCCAGGCTCC ACCGCGTGGC GCGCGACCTC	900
AAGTGGGCTAT GCATCGGACC GGTTCGCGGA AACCGGTTCC GCGGGGTCCG CTCATCGCTT	960
CATCCT	966

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

CGGCACCCGC GGCATACCG CCAGCGGAC CTTACCGCC GTTTCGCGG TTGCCCCCGT	60
TGCGCGCGCT CCGCGCGGCC CCGCGGATG AGTTCTCAT GCCAAAAGTA CTGGCGTTGC	120
CACCGAGGCG GCGTTGCGG CGGTACCGC CAGCCCGGCG GACTTCACCG GCGCCACCGA	180

CTCCGCGGCT GGCACGGTGG CCGCGGTTGG CGATCAACAT GCGGCTGGCG CCGCCCTTGC	240
CACCCACGCG ACCGGGTCGG CCGACCGCGC CGACACCAAG CGAGCTGCGG CCGGAGCCAC	300
CATCACCACC TACGCCACCG ACCGCCGAGA CCCCAGCGAC CGGCTCTTGG TGAAACGTGG	360
CGGTGCCACC ACCGCGCGCG TTACCGCCAA CCCCACCGCG AACCGCGCGG CCGGCATCCC	420
CGCGCGCGCG GCGGTTGCGG CGTTGCGCGC CGTTGCGGAA CAACAACCGG CCGGCGCGCG	480
CGTTGCGCGC CGCGCGCGCG GTCCGCGCGG CGCGCGCGAC GCGAGGCGCG CTGCGCGCGT	540
TGCGCGCATC ACCACCGTTG CCGCGGACCA CATCGGCTTC TGCGCGCGCG TCTGCGGTGT	600
CAAACTGCGC GATGCGAGCG TTGCGCGCGC TTGCGCGCGG CCGCGCGCGT CCGCGCTCAC	660
CACCGATACC ACCGCGCGCA CCGCGCGCAC CGTTGCGCGC ATCAGCGGAT AGCAACCGCG	720
CGCGCGCAC ATTCGCGCA GTTCCCGCGT CCGCACCGTC GCGCGCGGAG CCGGCACTGG	780
CAGCGCGCTT ACCACCGAAA CCGCGCGTAC CACCGGTAGA GGTGCGCGTG GCGATGTGTA	840
CGAAAGCGCG GCGTCCGCGG CCGCGCGTAC CACCGCGACT GCGCGCGCGT ACACCGTGGG	900
ACCGTTGCGT ACCATCACCG CCAAGCGCGC TCGCAATGTC GCGTGGCGCG ACTCGCGCGT	960
CGCGCGCGTT GCGCGCGCGG CCGCGCGGAG CCGCGGTACC GCGGTCAACA CCGGCAACCGC	1020
CGGTGCGCGT GCGGAGCGCT GCGTGGCGG TCGCACCGTC GCGCGCGGTG CCGCGCGTGG	1080
GCGTGGCGCG AGTGGCATGG CCGCGCGTGC CCGCGTGGCG GCGGTTTGA TCACCGATGC	1140
CGGACACATC TGCGCGCGTG TCGCGGTGC TCGCGCGCGG GCGCGCGTG GGATTGACCC	1200
CGTTGCGCGG GCGGAGCGCG GCGCGCGCGG TACGACCGCG GCGCGCATGG CCGAACAGCC	1260
CGCGTTGCGG GCGTTACCG CCGCACCGTC CGATGCGTGC GCGCACGCTG GTGCGCGCGA	1320
CACCGCGCTT GCGCGCGTTG CCGCACCAAC ACCCGCGCTT CCGACCGCGA CCGCGCGCGG	1380
CGCGGTACC ACCGCGCGCG CCGTTGCGCG CGTTGCGGAT CAACCGCGCG GCGCGTCCGC	1440
TGCGCGCGCT TTGACCGAAC CCGCGAGCGG CCGCGTTGCG ACCGTTGCGA AACAGCAACC	1500
CGCGCGCGCG GCGAGGCTGC CCGGTGCGCG TCGGTGCGCG GCGTTTTGCG ATCAACGCGC	1560
GCGCGAAAG GCGTGGGTG GCGCATTCG CCGCACCGAG CAGACTCGCG TCAACAGCGG	1620
CTTCACTGCT GCGATACCGA CCGCGCGCGG CAGTCAACCG CTGCACAAAC TGCTCGTGAA	1680
ACGCTGCCAC CTGTACGCTG AGCGCTGAT ACTGCGGAGC ATGGCGCGCG AACACCGCGG	1740
CAATCGCGCG CAGACTTCA TCGGAGCGCG CAGCCACCGC TTGCTGCTG CCGATCGCGG	1800
CGCGCGCATT AGCGCGCGTC ACCTGCGAAC CAGTACTCGA TAAATCCAAA GCGCGCTTGG	1860

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CCAGCAGCTG CCGCCTCCCG ATACCAAGG ACACCTGCA CCTCCGATA CCCCATATCG 1920
CCGCACCGTG TCCACAGCG CACCTGACC TTGCTGCTT GCTGCGCGG CCTGACTATG 1960
GCGCGACCGG CCTTCCTTCT GATTGCCCC GCGCGCGCAGC TTGTTGCGCG AGTTGAAGAC 2040
GGGAGGACAG GCGAGCTTG GTTAGACCT GGTCAAGTG GGAATGCACG GTCCCGCGCG 2100
AGATGAATAG GCGAGCGCG ATCTCCTTGT TGCTGASTCC CTCACCGACC AGTAGAGCCA 2160
CCTCAAGCTC TGTGGTGTG AACCGCCCC AGCCACTTGT CCGGCGTTTC CGTGACCGCG 2220
GGCCTCCTTG CCGTACCGG ATCGCTCAT CATCGATAA CCGAGTTCTT TCGGCCCCAGG 2280
CATGCTGAA CTGCTGTCA CCGATGATT TTGGAAGGCT GGTAGCGAC GAGTTACAGC 2340
CGCCCTGCTA GATCCGAGG CGGACCG 2367

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(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

```

Gln Pro Ala Gly Ala Thr Ile Ala Ala Ser Ser Pro Cys Ala Thr Val
1           5           10           15
Gly Ala Gly Gly Gly Thr Gly Ser Pro Val Thr Thr Glu Thr Ala Ala
20           25           30
Thr Thr Gly Arg Gly Gly Ser Gly Asp Val Tyr Glu Ser Ala Ala Ser
35           40           45
Gly Ala Ala Ala Thr Thr Pro Thr Ala Gly Gly Tyr Thr Val Gly Pro
50           55           60
Val Ala Thr Ile Thr Ala Lys Gly Ala Arg Asn Val Ala Leu Arg Asp
65           70           75           80
Ser Ala Val Ala Ala Val Ala Ala Ala Ala Thr Gly Ser Gly Gly Thr
85           90           95
Ala Val Thr Thr Gly Thr Ala Gly Gly Leu Ala Arg Ala Cys Arg Arg
100          105          110
Gly Gly Thr Val Ala Ala Gly Ala Thr Gly Arg Arg Ala Gly Ser Ala
115          120          125
Met Ala Ala Arg Ala Ala Val Ala Ala Gly Leu Ile Thr Asp Ala Gly
130          135          140

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His Ile Cys Arg Ala Val Pro Gly Ala Gly Arg Gly Ala Gly Arg Gly
 145 150 155 160
 Ile Asp Pro Val Cys Pro Gly Glu Ala Gly Ala Ala Gly Thr Thr Gly
 165 170 175
 Ala Ala Met Ala Glu Gln Pro Gly Val Ala Ala Val Thr Ala Arg Thr
 180 185 190
 Pro Asp Ala Cys Gly His Ala Gly Ala Ala Asp Thr Ala Val Ala Ala
 195 200 205
 Val Ala Pro Gln Pro Pro Pro Val Pro Thr Gly Thr Ala Gly Arg Ala
 210 215 220
 Gly Thr Thr Gly Pro Ala Val Ala Ala Val Ala Asp Gln Pro Gly Arg
 225 230 235 240
 Ala Ser Ala Ala Ala Gly Leu Thr Glu Pro Ala Ser Arg Ala Val Ala
 245 250 255
 Thr Val Ala Lys Gln Gln Pro Ala Gly Arg Ala Arg Leu Pro Gly Cys
 260 265 270
 Arg Pro Val Gly Ala Val Ser Asp Gln Arg Ala Pro Gln Lys Arg Leu
 275 280 285
 Gly Gly Arg Ile His Arg Thr Gln Gln Thr Pro Leu Asn Ser Gly Phe
 290 295 300
 Ser Ala Gly Xla Pro Thr Arg Gly Arg Ser Gln Arg Leu His Lys Leu
 305 310 315 320
 Leu Val Lys Arg Cys His Leu Tyr Ala Glu Arg Leu Ile Leu Pro Ser
 325 330 335
 Met Gly Pro Glu Gln Pro Arg Asn Arg Arg Arg His Phe Ile Gly Ser
 340 345 350
 Arg Ser His His Phe Arg Arg Arg Asp Arg Arg Gly Arg Ile Ser Arg
 355 360 365
 Ala His Leu Arg Thr Asn Ser Arg
 370 375

(2) INFORMATION FOR SEQ ID NO:203:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

GGCCAAAACG CCCCXGCGAT CCCCXCCACC GAGGCCGCGT ACGACCAGAT GTGGGCCCCAG	60
GACGTGGGCG CGATGTTTGG CTACCATGCC GGGGCTTCGG CGGCCGTCTC GGCCTTGACA	120
CGCTTCGGCC AGGCGCTGCC GACGCTGGCG GCGGGCGGTG CGCTGGTCAG CGCGGCCCGG	180
GCTCAGGTGA CCACGCGGCT CTPCCGCAAC CTGGGCTTGG CGAACGTCCG CGAGGSCAAC	240
GTCCSCAACG GTATGTTCGG GAATTTCAT CTGGGCTTCG CCAACATCGG CAACSSCAAC	300
ATCGGCAGCG GCAACATCGG CAGCTCCAC ATCGGGTTTG GCAACGTGGG TCCTGGGTTG	360
ACCGCAGCGC TGAACACAT CGGTTTCGCG AACACCGGCA GCAACACAT CGGTTTGGC	420
AACACCGGCA GCAACACAT CGGTTTCGCG AATACCGGAG ACGGCAACCG AGGTATCGGG	480
CTCAGCGGTA CGGTTTGTG GGGGTTCCGC GCGTGAACG CGGGCACCGG CAACATCGGT	540
CTGTTCAACT CCGGCACCGG AAACGTCCGC ATCGGCAACT CGGTACCGG GAACGCGGGC	600
ATTGSCAACT CGGGCAACAG CTACAACACC GGTTTTGGCA ACTCCGGGGA CCGCAACAG	660
GGCTTTCTCA ACTCGGAT AGGCAACACC GGCCTGGCA ACGCGGGCAA CTACAACACC	720
GGTAGCTACA ACCCGGGCAA CAGCAATACC GCGGCTTCA ACATGGGCAA GTACAACAG	780
GGCTACCTGA ACAGCGGCAA CTACAACACC GGCCTGGCAA ACTCCGGCAA TGTCAACACC	840
GGGCGCTTCA TTACTGGCAA CTCAACAAC GGCTTCTTGT GCGCGGGCAA CTACCAAGGC	900
CTGATTTTGG GGAGCGCGCG GTTCTTCAAC TCGACCACTG CGCGGTCTTC GGGATTCTTC	960
AACAGCGGTG CCGGTAGCGC GTTGGGCTTC CTGAACCTCG GTGCGAACAA TTCTGGCTTC	1020
TTCAACTCTT CTTGGGGGGC CATCGGTAAC TCGGGCTTGG CAACCGCGGG CTGCTGCTA	1080
TGCGGCGTGA TCAACTCGGG CAACACCTA TCGGTTTTGT TCAACATGAG CTTGGTGGC	1140
ATCACAACGC CGGCTTGGAT CTCGGGCTTC TTCAACACCG GAAGCAACAT GTGGGATTT	1200
TTGGGTGGCG CACCGGTCTT CAATCTCGGC CTGGCAAAAC GGGGCGTGGT GAACATTCTC	1260
GGCAACGCA ACATCGGCAA TTACAACATT CTCGGCAGCG GAACGTGGG TGACTTCAAC	1320
ATGTTTGGCA GCGGCAACCT CGGCAGGCAA AACATCTTGG GCAGCGGCAA CTTGGGAGC	1380
TTCAATATCG CAGTGGAAA CATCGGAGTA TTCAATGTG GTTCGGGAAG CTTGGGAAAC	1440
TACAACATCG CATCGGAAA CTTGGGATC TACAACATCG GTTTTGGAAA CTTGGGAGC	1500
TACAACGTG GTTTCGGGA GCGGGGCGAC TTCAACCAAG GCTTTGCCAA CACGGGCAAC	1560
AACAACATCG GTTGGGCAA CAGTGGCAAC AACAACATCG GATCGGGCT GTGGGGGAC	1620

AACCAGCAGG	GTTCAATAT	TGCTAGCGGC	TGGAACTCGG	GCACCGGCAG	CACCGGCTTG	1680
TTCAATTGCG	GCACCAATAA	CGTTGGCATC	TTCAACGCGG	GCACCGGAAA	CGTCGGCATC	1740
GCAAACTCGG	GCACCGGAAA	CTGGGGTATC	GGGAACCCCG	GTACCGACAA	TACCGGCATC	1800
CTCAATGCTG	GCAGCTACAA	CACGGGCTTC	CTCAACGCGG	GCGACTTCAA	CACGGGCTTC	1860
TACAACACCG	GCAGCTACAA	CACCGGCGGC	TTCAACGCTG	GTAACACCAA	CACCGGCAAC	1920
TTCAACGCTG	GTGACACCAA	TACCGGCGGC	TATAACCCCG	GTGACACCAA	CACCGGCTTC	1980
TTCAATCCCG	GCAACGTCAA	TACCGGCGCT	TTGACACCGG	GCGACTTCAA	CAATGGCTTC	2040
TTGGTGGCGG	GCGATAACCA	GGCCAGATT	GCCATCGATC	TCTGGGTGAC	CATCTCATTC	2100
ATCTTCATAA	ACGAGCAGAT	GTCATTGAC	GTACACAACG	TAATGACCTT	CGGCGGCAAC	2160
ATGATCAGCG	TCACCGAGGC	CTCGACCTT	TTCCCCAAA	CGTTCTATCT	GAGCGGTTTG	2220
TTCTTTCTCG	GCCCCGTCAA	TCTCAGCGCA	TCCACGCTGA	CGTTCCGAC	GATCACCTTC	2280
ACCATCGCGG	GACCGACGGT	GACCGTCCCG	ATCAGCATTC	TGGTGCTCT	GGAGAGCCCG	2340
ACGATTACCT	TCCTCAAGAT	CGATCCGCGG	CGGGGCATCG	GAAATTGGAC	CACCAACCCC	2400
TCGTCCGGCT	TTTTCAACTC	GGGCACCGGT	GGCACATCTG	GTTTCCAAA	CTTCGGCGGC	2460
GGCAGTTGAG	GCGTCTGAAA	CAGTGCTTTC	AGCAGCGCGA	TAGGGAATTC	GGGTTTCCAG	2520
AACCTCGGCT	CGGTCCAGTC	AGGCTGGGCG	AACCTGGGCA	ACTCCGTATC	GGGTTTCTTC	2580
AACACCGGTA	CGGTCAACCT	CTCCAGCGCG	GCCAAATGCT	CGGGCCTGAA	CAACATCGGC	2640
ACCAACCTGT	CGGGCCTGTT	CGCGGTCGG	ACCGGGAGGA	TTTTCAACGC	GGGCTTTGCC	2700
AACCTGGGCG	AGTTGAACAT	CGGCAGCGCG	TGCTGCCGAA	TTGGGCACGA	GTTAGATACG	2760
GTTTCAACAA	TCATATCGGC	GTTTGGCGGC	AGTGCATCAG	ACGAATCGAA	CCCGGGAAGC	2820
GTAAGCGAAT	AAACCGAATG	CGGGCTGCTC	AT			2852

(2) INFORMATION FOR SEQ ID NO:204:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 943 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Gly	Gln	Asn	Ala	Pro	Ala	Ile	Ala	Ala	Thr	Glu	Ala	Ala	Tyr	Asp	Gln
1				5					10					15	

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Met Trp Ala Gln Asp Val Ala Ala Met Phe Gly Tyr His Ala Gly Ala
 20 25 30

Ser Ala Ala Val Ser Ala Leu Thr Pro Phe Gly Gln Ala Leu Pro Thr
 35 40 45

Val Ala Gly Gly Gly Ala Leu Val Ser Ala Ala Ala Ala Gln Val Thr
 50 55 60

Thr Arg Val Phe Arg Asn Leu Gly Leu Ala Asn Val Arg Glu Gly Asn
 65 70 75 80

Val Arg Asn Gly Asn Val Arg Asn Phe Asn Leu Gly Ser Ala Asn Ile
 85 90 95

Gly Asn Gly Asn Ile Gly Ser Gly Asn Ile Gly Ser Ser Asn Ile Gly
 100 105 110

Phe Gly Asn Val Gly Pro Gly Leu Thr Ala Ala Leu Asn Asn Ile Gly
 115 120 125

Phe Gly Asn Thr Gly Ser Asn Asn Ile Gly Phe Gly Asn Thr Gly Ser
 130 135 140

Asn Asn Ile Gly Phe Gly Asn Thr Gly Asp Gly Asn Arg Gly Ile Gly
 145 150 155 160

Leu Thr Gly Ser Gly Leu Leu Gly Phe Gly Gly Leu Asn Ser Gly Thr
 165 170 175

Gly Asn Ile Gly Leu Phe Asn Ser Gly Thr Gly Asn Val Gly Ile Gly
 180 185 190

Asn Ser Gly Thr Gly Asn Trp Gly Ile Gly Asn Ser Gly Asn Ser Tyr
 195 200 205

Asn Thr Gly Phe Gly Asn Ser Gly Asp Ala Asn Thr Gly Phe Phe Asn
 210 215 220

Ser Gly Ile Ala Asn Thr Gly Val Gly Asn Ala Gly Asn Tyr Asn Thr
 225 230 235 240

Gly Ser Tyr Asn Pro Gly Asn Ser Asn Thr Gly Gly Phe Asn Met Gly
 245 250 255

Gln Tyr Asn Thr Gly Tyr Leu Asn Ser Gly Asn Tyr Asn Thr Gly Leu
 260 265 270

Ala Asn Ser Gly Asn Val Asn Thr Gly Ala Phe Ile Thr Gly Asn Phe
 275 280 285

Asn Asn Gly Phe Leu Trp Arg Gly Asp His Gln Gly Leu Ile Phe Gly
 290 295 300

Ser Pro Gly Phe Phe Asn Ser Thr Ser Ala Pro Ser Ser Gly Phe Phe

107

305 310 315 320

Asn Ser Gly Ala Gly Ser Ala Ser Gly Phe Leu Asn Ser Gly Ala Asn
325 330 335

Asn Ser Gly Phe Phe Asn Ser Ser Ser Gly Ala Ile Gly Asn Ser Gly
340 345 350

Leu Ala Asn Ala Gly Val Leu Val Ser Gly Val Ile Asn Ser Gly Asn
355 360 365

Thr Val Ser Gly Leu Phe Asn Met Ser Leu Val Ala Ile Thr Thr Pro
370 375 380

Ala Leu Ile Ser Gly Phe Phe Asn Thr Gly Ser Asn Met Ser Gly Phe
385 390 395 400

Phe Gly Gly Pro Pro Val Phe Asn Leu Gly Leu Ala Asn Arg Gly Val
405 410 415

Val Asn Ile Leu Gly Asn Ala Asn Ile Gly Asn Tyr Asn Ile Leu Gly
420 425 430

Ser Gly Asn Val Gly Asp Phe Asn Ile Leu Gly Ser Gly Asn Leu Gly
435 440 445

Ser Gln Asn Ile Leu Gly Ser Gly Asn Val Gly Ser Phe Asn Ile Gly
450 455 460

Ser Gly Asn Ile Gly Val Phe Asn Val Gly Ser Gly Ser Leu Gly Asn
465 470 475 480

Tyr Asn Ile Gly Ser Gly Asn Leu Gly Ile Tyr Asn Ile Gly Phe Gly
485 490 495

Asn Val Gly Asp Tyr Asn Val Gly Phe Gly Asn Ala Gly Asp Phe Asn
500 505 510

Gln Gly Phe Ala Asn Thr Gly Asn Asn Asn Ile Gly Phe Ala Asn Thr
515 520 525

Gly Asn Asn Asn Ile Gly Ile Gly Leu Ser Gly Asp Asn Gln Gln Gly
530 535 540

Phe Asn Ile Ala Ser Gly Trp Asn Ser Gly Thr Gly Asn Ser Gly Leu
545 550 555 560

Phe Asn Ser Gly Thr Asn Asn Val Gly Ile Phe Asn Ala Gly Thr Gly
565 570 575

Asn Val Gly Ile Ala Asn Ser Gly Thr Gly Asn Trp Gly Ile Gly Asn
580 585 590

Pro Gly Thr Asp Asn Thr Gly Ile Leu Asn Ala Gly Ser Tyr Asn Thr
595 600 605

Gly Ile Leu Asn Ala Gly Asp Phe Asn Thr Gly Phe Tyr Asn Thr Gly
 610 615 620
 Ser Tyr Asn Thr Gly Gly Phe Asn Val Gly Asn Thr Asn Thr Gly Asn
 625 630 635 640
 Phe Asn Val Gly Asp Thr Asn Thr Gly Ser Tyr Asn Pro Gly Asp Thr
 645 650 655
 Asn Thr Gly Phe Phe Asn Pro Gly Asn Val Asn Thr Gly Ala Phe Asp
 660 665 670
 Thr Gly Asp Phe Asn Asn Gly Phe Leu Val Ala Gly Asp Asn Gln Gly
 675 680 685
 Gln Ile Ala Ile Asp Leu Ser Val Thr Thr Pro Phe Ile Pro Ile Asn
 690 695 700
 Glu Gln Met Val Ile Asp Val His Asn Val Met Thr Phe Gly Gly Asn
 705 710 715 720
 Met Ile Thr Val Thr Glu Ala Ser Thr Val Phe Pro Gln Thr Phe Tyr
 725 730 735
 Leu Ser Gly Leu Phe Phe Phe Gly Pro Val Asn Leu Ser Ala Ser Thr
 740 745 750
 Leu Thr Val Pro Thr Ile Thr Leu Thr Ile Gly Gly Pro Thr Val Thr
 755 760 765
 Val Pro Ile Ser Ile Val Gly Ala Leu Glu Ser Arg Thr Ile Thr Phe
 770 775 780
 Leu Lys Ile Asp Pro Ala Pro Gly Ile Gly Asn Ser Thr Thr Asn Pro
 785 790 795 800
 Ser Ser Gly Phe Phe Asn Ser Gly Thr Gly Gly Thr Ser Gly Phe Gln
 805 810 815
 Asn Val Gly Gly Gly Ser Ser Gly Val Trp Asn Ser Gly Leu Ser Ser
 820 825 830
 Ala Ile Gly Asn Ser Gly Phe Gln Asn Leu Gly Ser Leu Gln Ser Gly
 835 840 845
 Trp Ala Asn Leu Gly Asn Ser Val Ser Gly Phe Phe Asn Thr Ser Thr
 850 855 860
 Val Asn Leu Ser Thr Pro Ala Asn Val Ser Gly Leu Asn Asn Ile Gly
 865 870 875 880
 Thr Asn Leu Ser Gly Val Phe Arg Gly Pro Thr Gly Thr Ile Phe Asn
 885 890 895

Ala Gly Leu Ala Asn Leu Gly Gln Leu Asn Ile Gly Ser Ala Ser Cys
 900 905 910

Arg Ile Arg His Glu Leu Asp Thr Val Ser Thr Ile Ile Ser Ala Phe
 915 920 925

Cys Gly Ser Ala Ser Asp Glu Ser Asn Pro Gly Ser Val Ser Glu
 930 935 940

(2) INFORMATION FOR SEQ ID NO:205:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GGATCCATAT GGCCCATCAT CATCATCATC ACCTGATCGA CATCATCGGG ACC

53

(2) INFORMATION FOR SEQ ID NO:206:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

CCTGAATTCA GGCTCGGTT GGCCCGGCT CATCTTGAAC GA

42

(2) INFORMATION FOR SEQ ID NO:207:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

GGATCCTGCA GGCTCGAAC CACCGAGCG ?

31

(2) INFORMATION FOR SEQ ID NO:208:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

CTCTGAATTC AGCCTTGGAA ATCCTCGCGA T

31

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GGATCCAGCG CTGAGATGAA GACCGATGCC GCT

33

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GGATATCTGC AGAATTCAGG TTAAAGCCC ATTTCGGA

38

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

CCGCATGCGA GGCACGTGCC CACACGGCC

39

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

CTTCATGGAA TTCTCAGGCC GGTAGGTCC GCTGCCG

37

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7675 base pairs
(B) TYPE: nucleic acid

201

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

TGGCGAATGG GACGCGCCCT GTAGCGGCCG ATTAAGCGCG GCGGGTGTGG TGGTTACGGG	60
CAGCGTGACC GCTACACTTG CCAGCGCCCT AGCGCGCGCT CATTGCGCTT TCTTCCCTTC	120
CTTCTCGCC ACCTTCGCGG GCTTTCCCGG TCAAGCTCTA AATCGGGGGC TCCCTTTAGG	180
GTTCCGATTY AGTGCTTTAC GGCACCTCGA CCCCCAAAAA CTTGATTAGG GTGATGGTTC	240
ACGTAGTGGG CCATCGCCCT GATAGACGGT TTTTCCCGCT TTAGCGTTGG AGTCCACGTT	300
CTTTAATAGT GGAATCTTGT TCCAAACTGG AACAACACTC AACCTATCT CCGTCCATTC	360
TTTGAATTGA TAAGCGATTY TCCCGATTTC GGCCTATTGG TTAATAAATG AGCTGATTGA	420
ACAAAAATTT AACCGGAATT TTAACAAAT ATTAACGTTT ACAATTTGAG GTGGCACTTT	480
TGGGGGAAT GTGGCGGCA CCGCTAATTC TTATTTTTC TAAATACATT CAAATATGTA	540
TCCGCTCATG AATTAATCT TAGAAAACT CATCGACAT CAAATGAAAC TCGAATTTAT	600
TCATATCGAG ATTATCAATA CCATATTTTT GAAAAAGCGG TTTCTGTAAAT GAAGGAGAAA	660
ACTCGCGGAG GCAATTCAT AGGATGGCAA GATCCTGCTA TCGGTCTGCG ATTCGGACTC	720
GTCCACATC AATACAACT ATTAATTTCC CCGCTCAAA AATAAGGTTA TCAAGTGAGA	780
AATCACCATE AGTGACCACT GAATCGGTG AGAATGGCAA AAGTTTATGC ATTTCTTCC	840
AGACTTCTTC AACAGGCCAG CCATTACCT CCGTCATCAA ATCACTCCCA TCAACCAAC	900
CGTTATTCAT TCGTATTTC GCGTGAGCGA GACGAAATAC GCGATCGCTG TTAAGAGGAC	960
AATTACAAC AGGAATCGAA TCGAACCGGC GCAGGAACAC TCCAGCGCA TCAACATAT	1020
TTTCACCTGA ATCAGGATAT TCTTCTAATA CCGGAATGC TGTTTTCCCG GCGATCCAG	1080
TGCTGAGTAA CCGTGCATCA TCAGGAGTAC GGATAAATG CTTGATGGTC GGAAGAGGCA	1140
TAAATTCCTT CAGCGAGTTT AGCTGACCA TCTCATCTGT AACATCATTC GCAACGCTAC	1200
CTTCCCATG TTTCAGAAAC AACTCTGGCG CATCGGCTT CCGATACAAT CGATAGATTG	1260
TGGACCTGA TTGCCCCGCA TTATCCGAG CCGATTTATA CCGATATATA TCAGCATCCA	1320
TGTTGGAATT TAATCGCGGC CTAGAGCAAG ACCTTTCCCG TTGAATATGG CTCATAACAC	1380
CCCTTGATTT ACTGTTTATG TAAGCAGACA GTTTTATTGT TCATGACCAA AATCCCTTAA	1440
CGTGAGTTT CTTCCACTG ACGCTCAGAC CCGTAGAAA AGATCAAAGG ATTTCTTTGA	1500

GATCCTTTT TTCTGCGCGT AATCTGCTGC TTGCAACAA AAAAACCACC GCTACCGCC	1560
GTGTTTTGTT TCCCGGATCA AGAGCTACCA ACTCTTTTTC CGAAGGTAAC TGGCTTCAGC	1620
AGAGCGCAGA TACCAATAC TCTCCTTCTA GTGTAGCCT AGTTAGGCCA CCACTTCAAG	1680
AACTCTGTAG CACCGCTAC ATACCTCGCT CTGCTAATCC TGTACCACT GCGTGTGCGC	1740
AGTGGCGATA AGTGTGTCT TACCGGTTG GACTCAAGAC GATAGTTACC GGATAAGGCC	1800
CACCGTCCG GCTGAACCG GGGTCTGTC ACACAGCCCA GCTTGGAGCG AACGACTTAC	1860
ACCGAAGTGA GATACCTACA GCCTGAGCTA TGAGAAAGCG CCACGCTTCC GGAAGCGAGA	1920
AAGGCGGACA GGTATCCGGT AAGCGGCGG GTCGGAACAG GAGAGCGCAC GAGGAGCTT	1980
CCAGCGGAA ACCCTGCTA TCTTTATAGT CCTGTGCGGT TTGCGCACTT CTGACTTGAG	2040
CGTGGATTTT TGTGATGCTC GTGAGGCGG CGAGCGCTAT GGAAGAACGC CAGCAACCG	2100
GCTTTTAC GTTCTGCGC CTTTGTGCG CTTTGTGCTC ACATGTTCTT TCTGCGTTA	2160
TCCCTGATT CTGTGATAA CGGTATTACC GCTTTGAGT GAGCTGATAC CGCTGCGCC	2220
AGCGAAGCA CCGAGCGCAG CGAGTCAGTG AGCGAGGAAG CGGAGAGCG CCGATGCGG	2280
TATTTCTCC TTACCATCT GTGCGTATT TCACACCGCA TATATGGTGC ACTCTCAGTA	2340
CAATCTGCTC TGATCCGCA TGTTAAGCC AGTATACCT CCGCTATCGC TACGTGACTG	2400
GCTCATGCT GCGCGCGAC ACCCGCCAC ACCCGTGC GCGCGCTGAC GCGCTTGTCT	2460
GCTCCCGCA TCGGTTACA GACAGCTGT GACCGTCTCC GCGAGCTGCA TGTGTCAGAG	2520
GTTTTCACCG TCATCACCGA AAGCGCGCAG GCAGCTGCGG TAAAGCTCAT CAGCTGCTC	2580
GTGAAGCAT TCACAGATGT CTGCGTCTC ATCGCGCTCC AGCTCCTTGA GTTTCTCCAG	2640
AAGCGTTAAT GTGTGCTTC TGATAAGCG GGCATGTTA AGGCGGTTT TTTCTGTTT	2700
GCTCACTGAT GCTCGCTGT AAGCGGAT TGTGTTCTG GGGTAATGA TACCGATGAA	2760
ACGAGAGAGG ATGCTCAGCA TACCGTTAC TGATGATGAA CATGCGCGCT TACTGGAACG	2820
TTGTAGCGGT AAACAAGTGG CGGTATGAT GCGCGCGGAC CAGAGAAAAA TCACTCAGGG	2880
TCAATGCCAG CGTTTCTTA ATACAGATGT AGGTGTTCCA CAGGTTAGCC AGCAGCATCC	2940
TGCGATGCG ATCGGAACA TAATGGTGA GCGCGCTGAC TTCCCGGTTT CCAGACTTTA	3000
CGAAACACCG AAACCGAAGA CCATTCTGT TGTGCTCAG GTGCGAGCG TTTGTCAGCA	3060
GCACTGCTT CAGTTGCTT CGGTATCGG TGATTGATC TCTAAGCAG TAAGGCAACC	3120
CCGCGAGCTT AGCGGCTCC TCAAGGACAG GAGCAGGATC ATGCGGACCC GTGGGCGCGC	3180

CATGCCCGCG AZAATGGGCT GCTTCTCGCC GAAAGCTTTG GTGGCGGGAC CAGTCACGAA	3240
GGCTTGAGCG AGGGCGTCCA AGATTCCGAA TACCGCAAGC GACAGGCGGA TCATCGTCCG	3300
GCTCCAGCGA AAGCGGTCTT CGCGGAAAT GACTCAGAGC GCTCGCGGCA CTTCTCTTAC	3360
GAGTTGCATG ATAAAGAAGA CAGTCATAAG TCGCGCGACG ATAGTCATGC CCGCGCGCCA	3420
CCGGAAGGAG CTGACTGGGT TGAAGCTCTT CAAGGGCATC GGTGAGATC CCGTGCCTA	3480
ATGAGTGAGC TAACTTACAT TAATTGCTTT GCGCTCACTG CCGCTTTTCC AGTCGCGAAA	3540
CCTGTCTGTC CAGCTGCATT AATGAATCGG CCAAGCGCGG GCGAGAGCGG GTTTCGCTAT	3600
TGCGCGCCAG GGTGCTTTT CTCTTCACCA GTGAGACGGG CAACAGCTGA TTGCTTTCA	3660
CGGCTGGCC CTGAGAGAGT TCGAGCAAGC GGTCCAGGCT GCTTTCGCCC AGCAGGCTAA	3720
AATGCTGTTT GATGCTGCTT AAGCGCGGAA TATAACATGA GCTGTCTTGG GTAGCTGCTT	3780
ATCCCACTAC CGAGATATCC GCACCAACGC GCAGCGCGGA CTCGCTAATG GCGCGCATTG	3840
CGCCAGCGCC CATCTGATCG TTGCAACCA GCTCGCGCTT GCGAAGCATG CCGTCATTCA	3900
GCAFTTGCAAT GCTTCTTGA AAACCGGACA TCGCACTCCA GTGCGCTTCC CGTTCGCTA	3960
TGCGCTGAAT TTGATTGCGA GTGAGATATT TATGCCAGCC AGCGAGACGC AGACGCGCCC	4020
AGACAGAACT TAATGCGCCG GCTAACAGCG CCAFTTGCTG GTGACCGAAT GCGACCTGAT	4080
GCTCCAGCGC CAGTGCCTA CCGCTCTTCT GCGAGAAAT AATCTGTTG ATGGTGTCTT	4140
GCTCAGAGAC ATCAAGAAAT AACGCGGAA CATTAGTCCA GCGAGCTTCC ACAGCAATCG	4200
CATCTGCTC ATCGAGCGGA TACTAATGA TCGCCCTACT GACGCTTTC GCGAGAAGAT	4260
TGTGACCGCC CGCTTACAG GCTTCAGCC CCGTTCTTTC TACCTCGAC ACCACCGCC	4320
TGGACCGCAG TTGATCGCCG CGAGATTGA TCGCCCGAC AATTGCGAC GCGCGCTGCA	4380
CGGCGAGACT GAGGCTGCA ACCCGAATCA GCAAGCACTG TTTGCGCGC AGTTGCTGTC	4440
CGACCGGTT GCGAATGTA TTGAGCTCCG CCACTCGCGC TTGCACTTTT TCGCGCTTT	4500
TGCGAGAAAC GTGGCTGCGC TCGTTCCCA CCGCGGAAAC GGTCTGATAA GAGACACCG	4560
CAGACTCTGC GACATGCTAT AACGTTACTG GTTTCACATT CACTACCTG AATTGACTTT	4620
CTTCGCGCGC CTATCATGCC ATACCGGAA AGGTTTTGCG CCAFTCGAGT GTGTCGCGA	4680
TCTGAGCGCT CTGCTTATG CCACTCTGCG ATTAGGAAGC AGCCCACTAG TAGCTTGAGG	4740
CGCTTGAGCA CCGCGCGCC AAGGAATGCT GCATGCAAGG AGATCGCGCC CAACATGCTT	4800

CCGCGCCACGG GGGCTGCCAC CATACCCACG CCGAAACAAG CGCTCATGAG CCGGAAGTGG	4880
CGAGCCCCGAT CTTCCCCATC GGTGATGTGG GCGATATAGG CCGCAGCAAC CCGACCTGTG	4920
GGCCCCGTGA TCCCCGCCAC GATCGCTCCG GCGTAGAGGA TCGAGATCTC GATCCCCCGA	4960
AATTAATACG ACTCACTATA GGGGAATTGT GAGCGGATAA CATTCCCCCT CTAGAAATRA	5040
TTTGTTTTAA CTTTAAGAAG GAGATATACA TATGGGCCAT CATCATCATC ATCAGCTGAT	5100
CGCATCATC GGGACCAAGC CCACATCTTG GGAACAGCGG CCGCGGAGG CGSTCCAGCG	5160
GGCGCGGAT AGCGTCGATG ACATCCGCTT CGCTCGGTC ATTGAGCAGG ACATGGCCCT	5220
GGACAGCGCC GCGAAGATCA CCTACCGCAT CAAGCTCGAA GTGTGTTTCA AGATGAGGCC	5280
GGCGCAACCG AGGGGCTCGA AACTACCGAG CGTTCCGCTT GAAACCGGGG CCGCGCCCGG	5340
TACTGTCCCG ACTACCGCGG CTTGCTCGCC GGTGACGTTG GCGGAGACCG GTAGCAGGCT	5400
GCTTACCGG CTGTTCAACC TGTGGGTTCC GGCCTTTCAC GAGAGGTATC CGAACCTCAC	5460
GATCACCGCT CAGGGCACCG GTTCTGCTTC CCGGATCGCG CAGGCGCGCG CCGGACCGGT	5520
CAACATTGGG GCTCCGACG CCTATCTGTC GGAAGGTGAT ATGGCGCGGC ACAAGGGGCT	5580
GATGAACATC GCGCTAGCCA TCTCCGCTCA GCAAGTCAAC TACAACCTTC CCGAGTGAAG	5640
CGAGCACCTC AAGCTGACG GAAAATCTCT GCGCGCCATG TACCAAGGCA CCGTCAAAAC	5700
GTGGACGAC CCGCAGATCG CTGCGCTCAA CCGCGCGTG AACTTGGCGG GACCGCTGCT	5760
AGTTCCGCTG CACCGCTCCG ACGGCTCCCG TGACACCTTC TTGTTACCC AGTACCTGTC	5820
CAAGCAAGAT CCGAGGCTT GGGGCAAGTC GCGCGCTTC GGCACCAAGG TCGACTTCCC	5880
GGCGGTGCGG GTTGCCTTGG GTGAGAACCG CAACGGCGGC ATGCTGACCG GTTGGCGCGA	5940
GACACCGGCG TCGTGGCTT ATATCGGCT CAGCTTCTTC GACCAAGGCA GTCAACGGGG	6000
ACTCGGCGAG GCGCAACTAG GCAATAGCTC TGCAATTTC TTGTTGCGCG ACGCGCAAG	6060
CATTCAAGCC GCGCGGCTG GCTTGGCATC GAAAACCCCG GCGAACCAGG CGATTTCGAT	6120
GATCGACCGG CCGCGCGCGG ACGGCTACCG GATCATCAAC TACGAGTACG CCATCTCTAA	6180
CAACCGGCAA AAGGACGCTG CCGCGCGCA GACCTTGCAG GCATTTCTTC ACTGGGCGAT	6240
CACCGACGCG AACAGGCTT GTTCTCTGCA CCGAGTTTCA TTCCAGCGCG TGCCGCGCGC	6300
GGTGGTGAAG TTGTCTGACG GTTGATCTC GACGATTTCC AGCGCTGAGA TGAAGACCGA	6360
TGCGGCTACC CTCGCGCAGG AGGCAAGTAA TTTCAGCGCG ATCTCGGCGG ACCTGAAAAC	6420
CGAGATCGAC CAGGTGAGT CCGCGCGAGG TTCTTTCAG GCGAGTGGC GCGCGCGCGC	6480

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GGGAGAGGCG GCGCAGGCGG CGGTGGTGGG CTTCGAAGAA GCAGCCAATA AGCAGAAGCA 6540
GGAACTCGAC GAGATCTCGA CGAATATTCG TCAGGCGCGG GTCCAATACT CGAGGCGCGA 6600
CGAGGAGCAG CAGCAGGCGG TGTGCTCGCA AATGGGCTTT GTGCGGCACAA CGGCGGCGTC 6660
GCGGCGGTGG ACCGCTGCGG CGCCACCGCG ACCGCGGACA CCTGTGCGCG CCGCAGCAGC 6720
GGCGCGTGGG AACACGCGCA ATGCGCGCGG GGGCGATCGG AACCGAGCAC CTCGCGCGCG 6780
CGACCGGAAC GCACCGCGCG CACCTGTGAT TGCGCGCAAC GCACCGCAAC CTGTGCGGAT 6840
CGACAACCGG GTTGGAGGAT TCAGCTTGGG GCTGCGTGGT GGTGCGGTGG AGTGTGAGCG 6900
CGCGCACTTC GACTACGGTT CAGCACTCGT CAGCAAAACC ACCGCGGAGC CGCGCTTTCG 6960
CGGACAGCGG CGCGCGGTGG CGCATGACAC CGTATCGTGG CTGCGCGCGG TAGACCAAAA 7020
GCTTTACGGG AGCGCGGAAG CCACCGACTC CAAGCGCGCG GCGCGGTGGG GCTCGGACAT 7080
GGGTGAGTTC TATATCGGCT ACCGCGGCGC CGGATCAAC CAGGAAACCG TCTCGCTTGA 7140
CGCGACCGGG GTGTCTGGA GCGCTGCTGA TTACGAAGTC AAGTTCAGCG ATCCGAGTAA 7200
GCGGAACCGC CAGATCTCGA CGCGCGTAAT CGGCTCGCGG GCGCGGAAGC CACCGGAGCG 7260
CGCGCGCGCGT CAGCGCTGGT TTGTGCTATG GCTCGGGAGC GCGCAACGAC CGGTGGACAA 7320
GGGCGCGCGG AAGCGCGTGG CGAATCGAT CGCGCGTTTG GTCGCGCGCG CGCGCGCGCG 7380
GGCAGCGGCT CCGCAGAGG CGCTCGCGC GCGCGCGCGG GCGCGGGAAG TCGCTCTTAC 7440
CGCGAGCACA CGGACAGCGC AGCGGAGCGT ACDSGCGTGA GAATTCGCA GATATCGATC 7500
ACACTGCGCG CGGCTCGAGC ACCACGACCA CCACCACTGA GATCGCGCTG CTAACGAAGC 7560
CGGAAAGGAA GCTGAGTTGG CTGCTGCGAC CGCTGAGCAA TAAGTAGCAT AACCGCTGG 7620
GGCTCTTAAA CGGCTCTTGA GCGGTTTTTT GCTGAAAGGA GGAAGTATAT CGGAT 7676

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(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 802 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

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Met Gly His His His His His Val Ile Asp Ile Ile Gly Thr Ser
1           5           10           15
Pro Thr Ser Trp Glu Gln Ala Ala Ala Glu Ala Val Gln Arg Ala Arg

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206

20	35	50
Asp Ser Val Asp Asp Ile Arg Val Ala Arg Val Ile Glu Gln Asp Met		
35	40	45
Ala Val Asp Ser Ala Gly Lys Ile Thr Tyr Arg Ile Lys Leu Glu Val		
50	55	60
Ser Phe Lys Met Arg Pro Ala Gln Pro Arg Gly Ser Lys Pro Pro Ser		
65	70	75
Gly Ser Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro		
85	90	95
Ala Ser Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr		
100	105	110
Pro Leu Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn		
115	120	125
Val Thr Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln		
130	135	140
Ala Ala Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser		
145	150	155
Glu Gly Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala		
160	165	170
Ile Ser Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His		
180	185	190
Leu Lys Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile		
195	200	205
Lys Thr Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn		
210	215	220
Leu Pro Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly		
225	230	235
Asp Thr Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly		
240	245	250
Trp Gly Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val		
255	260	265
Pro Gly Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys		
270	275	280
Ala Glu Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp		
285	290	295
Gln Ala Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser		
300	305	310
		315
		320

Gly Asn Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala
 325 330 335
 Gly Phe Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp
 340 345 350
 Gly Pro Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile
 355 360 365
 Val Asn Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala
 370 375 380
 Phe Leu His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp
 385 390 395 400
 Gln Val His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp
 405 410 415
 Ala Leu Xle Ala Thr Ile Ser Ser Ala Glu Met Lys Thr Asp Ala Ala
 420 425 430
 Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile Ser Gly Asp Leu
 435 440 445
 Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly
 450 455 460
 Glu Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg
 465 470 475 480
 Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile Ser
 485 490 495
 Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu Glu
 500 505 510
 Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe Val Pro Thr Thr Ala
 515 520 525
 Ala Ser Pro Pro Ser Thr Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro
 530 535 540
 Val Ala Pro Pro Pro Pro Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro
 545 550 555 560
 Gly Asp Pro Asn Ala Ala Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro
 565 570 575
 Pro Pro Val Ile Ala Pro Asn Ala Pro Gln Pro Val Arg Ile Asp Asn
 580 585 590
 Pro Val Gly Gly Phe Ser Phe Ala Leu Pro Ala Gly Trp Val Glu Ser
 595 600 605

Asp Ala Ala His Phe Asp Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr
 610 615 620
 Gly Asp Pro Pro Phe Pro Gly Gln Pro Pro Pro Val Ala Asn Asp Thr
 625 630 635 640
 Arg Ile Val Leu Gly Arg Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu
 645 650 655
 Ala Thr Asp Ser Lys Ala Ala Ala Arg Leu Gly Ser Asp Met Gly Glu
 660 665 670
 Phe Tyr Met Pro Tyr Pro Gly Thr Arg Ile Asn Glu Glu Thr Val Ser
 675 680 685
 Leu Asp Ala Asn Gly Val Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys
 690 695 700
 Phe Ser Asp Pro Ser Lys Pro Asn Gly Gln Ile Trp Thr Gly Val Ile
 705 710 715 720
 Gly Ser Pro Ala Ala Asn Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp
 725 730 735
 Phe Val Val Trp Leu Gly Thr Ala Asn Asn Pro Val Asp Lys Gly Ala
 740 745 750
 Ala Lys Ala Leu Ala Glu Ser Ile Arg Pro Leu Val Ala Pro Pro Pro
 755 760 765
 Ala Pro Ala Pro Ala Pro Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala
 770 775 780
 Gly Glu Val Ala Pro Thr Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu
 785 790 795 800
 Pro Ala

(2) INFORMATION FOR SEQ ID NO:215:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION:- SEQ ID NO:315:

GTGGCGGCGC	TGCGGCGGCG	CAGCAGAGCG	ATGTGCATCG	GTTCGCGGAAC	CTGATCGGCG	60
TCGACGATGA	GCGCGCGGAA	CGCGGCGGAG	ACGAGAGAGC	TCAGGAAGCC	GTCCAGCAGC	120
GCGGTGCGCG	CGGTGAGGAA	GCTGAGCGCG	TGCGAGATCA	GCAGCAGCCC	GGCGATGCGG	180
CGGACCAATG	TCGACCGGCT	GATCGGCGCG	ACGATCGGCA	CCAGCAGCGC	CACGAGGACC	240
ACACCGAGCA	GCGCGCGGCT	GAACCGGCGG	CGGATCGGCT	TGTGACCGAA	GATCGGCGCT	300


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CCGATCGCGA TCAGCTGCTT ACCGACCGGC GGGTGAACCA CAGGCGCGTA CCGGGGTTG 360
TCTTCCACCC CATGGTTGTT CAGCACCTGC CAGGCGTGGC GGTGGCTAAT GCTTCTGCTC 420
GAAGATCGGG GTGCGGGCAT CCGTACCGA GCCC

```

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 470 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

```

TGCAGAACTA CCGCGGATTC TCGTGGCGG AGCGCGAAGC GATTCCCGCC GTCGCGAAG 60
GCATCGTCCG CAGCAAGAAG CAAGGCAATG ACCTCGTCCT CCGTCTCTCT GCGATGGGGG 120
ATACCAACCGA CAGCTGCTG GATCTGGCTC AGCAGTCTG CCGCGCGCGG CCGCGTGGGG 180
AGCTGGACAT GCTGCTTACC GCGGTGAAC GCATCTCGAA TCGCTTGCTG GCCATGGCCA 240
TCAGTGGCT CCGCGCGCAT GCGCGTCTT TCGCGCTTC GCAGGCGCGG GTCATCAGCA 300
CGGCGACCCA CGGCAACGGC AAGATCATCG AGTCAAGCC GGGGCGGCTG CAAACCGGCC 360
TTGAGGAAGG GCGGCTCTG TTGGTGGCGG GATTCCAAGG GGTCAAGCCAG GACACCAAGG 420
ATGTCAGGAC GTTGGGCGCG GCGGCTCGG ACACCAAGC GTCGCGCATG 470

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(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

```

GGCGCGCGTA CCGCGCGGG ACAAACRAG ATCGATTGAT ATCGATGAGA GACGAGGAA 60
TCTGGGCTT TCCCAAGTT ACCGACGAGC AGCGCGCGG CCGCTTGGAG AAGGCTGCTG 120
CGGCACTCG AGCGGAGCA GAGTCAAGG ATCGGCTCA GCGTGGCGGC ACCAAGCTCA 180
CCGAGTCTT CAAGGACCG GAGAGCGATG AAGTCTTGG CAAATGAAG GTGTCTGCGC 240
TGCTTGAGGC CTTCCTAAG GTGGCAAGG TCCAGGCGC

```

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

ACACGGTCCA	ACTCGACGAG	CCCCCTCGTGG	AGGTGTCGAC	CGACAAGGTC	GACACCGAAA	60
TCCCTCGCCG	GCCGCGGGTG	TGCTGACCAA	GATCATCGCC	CRAGAAGATG	ACACGGTCCA	120
GGTCGGCGGC	GAGCTCTCTG	TCATTGGCGA	CGCCCATGAT	GCCGGCGAGG	CCGCGGTCCC	180
GSEACCCGAG	AAAGTCTCTG	CCGCCCCAAC	CGAATCCA			219

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TGGTTCGCGA	CATCGGCGCC	GCGCGCGCCC	CCAAGCCCGC	ACCCAGGCCC	GTCCCGGAGC	60
CAGCGCGGAC	GCCGAGGGCC	GAACCGGCAC	CATCGCGGCC	GGCGGCGGAG	CCAGCGGCTG	120
CGGCGGAGGG	CGCACCGTAC	GTGACCGCCC	TGGTCCGAAA	GCTGGCGCTG	GAAACGACAC	180
TGGACCTCGC	CGGGGTGACT	GGCACCGGAG	TGGTGGCTCG	CATCGCGAAA	CAGGATGTGC	240
TGGCGCGCGC	TGAACAAAAG	AAGCGGCGCA	AAGCACCGGC	GCGGCGCGCC	CAGGCGGCGC	300
CCGCGCGCGC	CCGGAAGGCG	CGGCTGAAG	ATCGGATGCC	GC		342

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

GGGTCTTGGT	CAGTATCAGC	GCCGACGAGG	ACCCGACGGT	GCCCCTCGGC	GGCGAGTTGG	60
CCCGGATCGG	TGTGCTGCCC	GACATCGGCG	CCCGCGCGGC	CCCCAAGCCC	GCACCCAGGC	120
CCGTCCCCGA	GCCAGCGGCC	ACGCGGAGG	CCGAACCGCC	ACCATCGCCG	CCGGCGGCCC	180
AGCCAGCGCG	TGCGGCGGAG	GGCGCACCGT	ACGTGACGCC	GCTGGTGCGA	AAGCTGGCGT	240
CGGAAACAAA	CATCGACCTC	GCCGGGGTGA	CCCGGACCGG	AGTGGGTGGT	CGCATCGCGA	300
AACGGGATGT	GCTGGCGCGG	GCTGAACAAA	AGAAGCGGGC	GAAAGCACCG	GCGCCCTGAG	360
CCCTTCATCA	CCCGGTTAAC	CAGCTTGCCC	CAGAAGCGCG	CTTCGACCTC	TTGCGCGGTC	420
TTGGTCCGCT	GCAGGCGGTC	GGCGAGCCAG	TTGAGGTTAG	GCGGCGGAAA	TCTTCCAGTT	480
CCCGAGGAAG	GCGACCCCGA	ACAGGTTCCG	CACCC			515

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

CCGACCCCAA	GGTGCAGATT	CAACAGGCCA	TTGAGGAAGC	ACAGCGCACC	CACCAAGCSC	60
TGACTCAACA	GGCGGCCCAA	GTGATCGGTA	ACCAGCGTCA	ATTGGAGATG	CGACTCAACC	120
GACAGCTGCC	GGACATCSAA	AAGCTTCAGG	TCAATGTGCG	CCAAGCCCTG	ACGCTGCCCG	180
ACCAGGCCAC	CGCCGCCGGA	GAGGCTGCCA	AGGCCACCGA	ATACAACAC	GGCGCCGAGG	240
CGTTCCGAGC	CCAGCTGGTG	ACCGCCGAGC	AGAGCGTCCA	AGACCTCAAG	ACGCTGCATG	300
ACCAGGCGCT	TAGCGCCGCA	GCTCAGGCCA	AGAAGGCCGT	CGAACGAAAT	GGGATGGTGC	360
TGCAGCAGAA	GATCGCCGAG	CGAACCAGC	TGCTCAGCCA	GCTCGAGCAG	GGGAAGATGC	420
AGGAGCAGGT	CAGCGCATCG	TTGCGGTCCA	TGAGTGAGCT	CGCCGCGCCA	GGCAACACGC	480
CGAGCCTCGA	CGAGGTCCGC	GACAAGATCG	AGCGTCGCTA	CGCCAACGCG	ATCGGTTCCG	540
CTGAACCTTC	CGAGAGT					587

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

CAGGATAGGT	TTGACATCC	ACCTGGGTTG	CGCAGCCGGT	GCGCGACCGT	GTGATAGGCC	60
AGAGGTGGAC	CTGCGGCCAG	CGACGATCGA	TGAGGAGTTC	AACAGAAATG	GCCTTCTCCG	120
TCCAGATGCC	GGCACTCGGT	GAGAGGCTCA	CGAGGGGAC	GCTTACCCGC	TGGCTCAAAC	180
AGGAAGGCCA	CACGGTCCGA	CTCGACGAGC	CCCTCGTGGA	GCT		223

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

AAGAAGTACA	TCTGCCGGTC	GATGTGGGCG	AACCACGGCA	GCCAACCGGC	GCAGTAGCCG	60
ACCAGGACCA	CCGCATACG	CCAGTCCCGG	CSCACAAACA	TACGCCACCC	CGGCTATGCC	120
AGGACTGGCA	CGCCAGGCCA	CCACATCCCG	GGCGTGCGGA	CCAGCATCTC	GGCCTTGACG	180
CACGACTGTG	CGCCGACGCT	TGCAACCTCT	TCCTGGTCCA	TGSCCTACAG	CACCGGCCGC	240
AACGACATGG	GCCAGGTCCA	CGCTTTGGAT	TCCCAAGGGT	GCTAGTTGCC	TGCCGAATTC	300
GTGAGCCCCG	CGTGGAAAGTG	GAACGCTTTG	GCGGTGTATT	GCCAGAGCGA	CGGCACGCGG	360
TGCGGCAGCG	GAACAAACGA	GTTGCGACCG	ACCGCTTGAC	CGACCGCATG	CCGATCGATC	420
GCGGTCTCGG	ACCGGAACCA	CGGAGCGTAG	GTGCCCAGAT	AGACCGCGAA	CGGGATCAAC	480
CCGAGCGCAT	ACCGGCTGGG	AAGCACGTCA	CGCGGCACTG	TTCCCAAGCA	CGGTCTTTGC	540
ACTTGGTATG	AACGTGGGCG	CGCCACGTCA	ACGCCAGC			578

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

ACAACGATCG	ATTGATATCG	ATGAGAGACG	GAGGAATCGT	GGCCCTTCCC	CAGTTGACCG	50
ACGAGCAGCG	CCCGGCCGCG	TTGGAGAAGG	CTGCTGCGGC	ACGTGCGAGC	CGAGCAGAGC	120
TCAAGGATCG	GCTCAAGCGT	GGCGGCACCA	ACCTCACCCA	GGTCTCTCAAG	GACCGGGAGA	180
GCGATGAAGT	CTTGGGCAAA	ATGAAGGTGT	CTGCCCTGCT	TGAGGCTTTG	CCAAAGGTGG	240
GCAAGGTCAA	GGCCAGGAG	ATCATGACCG	AGCTGGAAT	TGCCGCCAC	CCCGCGCGCT	300
TCTGGGCTTC	GGTGACCGTC	AGCCCAAGGC	CTTGCTGGAA	AAGTTGGCT	CCGCTTAACC	360
CCGCTGGCGC	ACGATGGGG	CCGGAAGGCC	TGTGGTGGGC	GTACCCCGGC	ATACGGGGGA	420
GAAGCGCGCT	GACAGGGCCA	GCTCACAATT	CAGGCCGAAC	GGCCCGGTGG	GGGGGAACCC	480
GGCC						484

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

AGGACTGGCA	CCGCCAGCCA	CCACATCGCG	GGCGTGCCGA	CCAGCATCTT	GGCCTTGACC	50
CACGACTGTG	CGCGGCAGCT	TGCAACGTGT	TGCTGGTGGG	TGGCGTACAG	CACCGGCGGC	120
AACGACATGG	GCGAGGTCCA	CGGTTTGGAT	TCCCAAGGGT	GGTAGTTGCC	TGCGGAATTC	180
GTCAAGGCGCG	CGTGGAACTG	GAACGCTTTG	GGCGTTTAACT	GCCAGAGCCA	GCGCACGGCG	240
TCCGGCAGCG	GAACACCCA	GTTGCGACCG	ACCGCTTGAC	CGACCGCATG	CCGATCGATC	300
CGGGTCTCGG	ACCGCAACCA	CGGAGCGTAG	GTGGCCGAT	AGACCGCGAA	CGGGATCAAC	360
CCGAGCGCAT	ACCGCTGGG	AAGCACCTCA	CGCCGCACTG	TCCCGAGCCA	CGGTCTTTGC	420
ACTTGCTACT	GACGTGCGGC	CGCCACCTCG	AACGCCAGCG	CCATCGCGCC	GAAGAACAGC	480
ACGAAGTACA	CGCCGACCA	CTTGCTGGCG	CAAGCCAATC	CCAAGCAGCA	CCCCGGC	537

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

213

Gly Gly Ala Ala Ala Gly Gln Gln Ser Asp Val His Pro Phe Ala Asn
 1 5 10 15
 Leu Ile Ala Val Asp Asp Glu Arg Ala Glu Arg Arg Asp Asp Glu Gln
 20 25 30
 Arg Gln Glu Ala Val Gln Gln Arg Gly Pro Arg Gly Asp Glu Ala Asp
 35 40 45
 Pro Val Ala Asp Gln Gln His Pro Gly Asp Gly Ala Asp Gln Cys Arg
 50 55 60
 Pro Ala Asp Pro Pro His Asp Pro His His Gln Arg His Gln Asp His
 65 70 75 80
 Thr Gln Gln Gly Ala Gly Glu Pro Pro Ala Glu Ser Val Val Thr Glu
 85 90 95
 Asp Gly Leu Pro Asp Arg Asp Gln Leu Leu Thr Asp Arg Arg Val Asn
 100 105 110
 His Gln Ala Val Pro Gly Val Val Phe His Pro Met Val Val Gln His
 115 120 125
 Leu Pro Gly Leu Ala Val Arg
 130 135

(2) INFORMATION FOR SEQ ID NO:227:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 156 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Gln Lys Tyr Gly Gly Ser Ser Val Ala Asp Ala Glu Arg Ile Arg Arg
 1 5 10 15
 Val Ala Glu Arg Ile Val Ala Thr Lys Lys Gln Gly Asn Asp Val Val
 20 25 30
 Val Val Val Ser Ala Met Gly Asp Thr Thr Asp Asp Leu Leu Asp Leu
 35 40 45
 Ala Gln Gln Val Cys Pro Ala Pro Pro Pro Arg Glu Leu Asp Met Leu
 50 55 60
 Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu Val Ala Met Ala Ile
 65 70 75 80
 Glu Ser Leu Gly Ala His Ala Arg Ser Phe Thr Gly Ser Gln Ala Gly
 85 90 95
 Val Ile Thr Thr Gly Thr His Gly Asn Ala Lys Ile Ile Asp Val Thr
 100 105 110
 Pro Gly Arg Leu Gln Thr Ala Leu Glu Glu Gly Arg Val Val Leu Val
 115 120 125
 Ala Gly Phe Gln Gly Val Ser Gln Asp Thr Lys Asp Val Thr Thr Leu
 130 135 140
 Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala Met
 145 150 155

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

```

Pro Ala Tyr Pro Ala Gly Thr Asn Asn Asp Arg Leu Ile Ser Met Arg
 1           5           10           15
Asp Gly Gly Ile Val Ala Leu Pro Gln Leu Thr Asp Glu Gln Arg Ala
 20           25           30
Ala Ala Leu Glu Lys Ala Ala Ala Arg Arg Ala Arg Ala Glu Leu
 35           40           45
Lys Asp Arg Leu Lys Arg Gly Gly Thr Asn Leu Thr Gln Val Leu Lys
 50           55           60
Asp Ala Glu Ser Asp Glu Val Leu Gly Lys Met Lys Val Ser Ala Leu
 65           70           75           80
Leu Glu Ala Leu Pro Lys Val Gly Lys Val Gln Ala
 85           90

```

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

```

Thr Val Glu Leu Asp Glu Pro Leu Val Glu Val Ser Thr Asp Lys Val
 1           5           10           15
Asp Thr Glu Ile Pro Ser Pro Ala Ala Gly Val Leu Thr Lys Ile Ile
 20           25           30
Ala Gln Glu Asp Asp Thr Val Glu Val Gly Gly Glu Leu Ser Val Ile
 35           40           45
Gly Asp Ala His Asp Ala Gly Glu Ala Ala Val Pro Ala Pro Gln Lys
 50           55           60
Val Ser Ala Gly Pro Thr Arg Ile
 65           70

```

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

```

Ala Ala Asp Ile Gly Ala Ala Pro Ala Pro Lys Pro Ala Pro Lys Pro
 1           5           10           15
Val Pro Glu Pro Ala Pro Thr Pro Lys Ala Glu Pro Ala Pro Ser Pro
 20           25           30
Pro Ala Ala Glu Pro Ala Gly Ala Ala Glu Gly Ala Pro Tyr Val Thr
 35           40           45
Pro Leu Val Arg Lys Leu Ala Ser Glu Asn Asn Ile Asp Leu Ala Gly
 50           55           60
Val Thr Gly Thr Gly Val Gly Gly Arg Ile Arg Lys Glu Asp Val Leu
 65           70           75           80
Ala Ala Ala Glu Glu Lys Lys Arg Ala Lys Ala Pro Ala Pro Ala Ala
 85           90           95
Gln Ala Ala Ala Ala Pro Ala Pro Lys Ala Pro Pro Glu Asp Pro Met
100           105           110
Pro

```

(2) INFORMATION FOR SEQ ID NO:231:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

```

Val Leu Val Ser Ile Ser Ala Asp Glu Asp Ala Thr Val Pro Val Gly
 1           5           10           15
Gly Glu Leu Ala Arg Ile Gly Val Ala Ala Asp Ile Gly Ala Ala Pro
 20           25           30
Ala Pro Lys Pro Ala Pro Lys Pro Val Pro Glu Pro Ala Pro Thr Pro
 35           40           45
Lys Ala Glu Pro Ala Pro Ser Pro Pro Ala Ala Glu Pro Ala Gly Ala
 50           55           60
Ala Glu Gly Ala Pro Tyr Val Thr Pro Leu Val Arg Lys Leu Ala Ser
 65           70           75           80
Glu Asn Asn Ile Asp Leu Ala Gly Val Thr Gly Thr Gly Val Gly Gly
 85           90           95
Arg Ile Arg Lys Glu Asp Val Leu Ala Ala Ala Glu Glu Lys Lys Arg
100           105           110
Ala Lys Ala Pro Ala Pro
115

```

(2) INFORMATION FOR SEQ ID NO:232:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 135 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

```

Asp Pro Lys Val Gln Ile Gln Gln Ala Ile Glu Glu Ala Gln Arg Thr
 1           5           10           15
His Gln Ala Leu Thr Gln Gln Ala Ala Gln Val Ile Gly Asn Gln Arg
 20           25           30
Gln Leu Glu Met Arg Leu Asn Arg Gln Leu Ala Asp Ile Glu Lys Leu
 35           40           45
Gln Val Asn Val Arg Gln Ala Leu Thr Leu Ala Asp Gln Ala Thr Ala
 50           55           60
Ala Gly Asp Ala Ala Lys Ala Thr Glu Tyr Asn Asn Ala Ala Glu Ala
 65           70           75           80
Phe Ala Ala Gln Leu Val Thr Ala Glu Gln Ser Val Glu Asp Leu Lys
 85           90           95
Thr Leu His Asp Gln Ala Leu Ser Ala Ala Gln Ala Lys Lys Ala
100          105          110
Val Glu Arg Asn Ala Met Val Leu Gln Gln Lys Ile Ala Glu Arg Thr
115          120          125
Lys Leu Leu Ser Gln Leu Glu Gln Ala Lys Met Gln Glu Gln Val Ser
130          135          140
Ala Ser Leu Arg Ser Met Ser Glu Leu Ala Ala Pro Gly Asn Thr Pro
145          150          155          160
Ser Leu Asp Glu Val Arg Asp Lys Ile Glu Arg Arg Tyr Ala Asn Ala
165          170          175
Ile Gly Ser Ala Glu Leu Ala Glu Ser
180          185

```

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

```

Val Ser Thr Ser Thr Trp Val Pro His Pro Val Arg Asp Arg Val Ile
 1           5           10           15
Gly Gln Arg Trp Thr Cys Ala Asp Arg Arg Ser Ile Glu Glu Ser Thr
 20           25           30
Glu Met Ala Phe Ser Val Gln Met Pro Ala Leu Gly Glu Ser Val Thr
 35           40           45
Glu Gly Thr Val Thr Arg Trp Leu Lys Gln Glu Gly Asp Thr Val Glu
 50           55           60
Leu Asp Glu Pro Leu Val Glu
 65           70

```

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

```

Glu Val His Leu Pro Val Asp Val Gly Glu Pro Arg Gln Pro Thr Gly
 1           5           10           15
Ala Val Ala Asp Gln Asp His Arg Ile Thr Pro Val Pro Ala His Lys
 20           25           30
His Thr Pro Pro Arg Val Cys Gln Asp Trp His Arg Gln Pro Pro His
 35           40           45
Arg Gly Arg Ala Asp Gln His Leu Gly Leu Asp Ala Arg Leu Cys Ala
 50           55           60
Ala Ala Cys Asn Val Leu Leu Val Asp Gly Val Gln His Arg Pro Gln
 65           70           75           80
Arg His Gly Pro Gly Pro Arg Phe Gly Phe Pro Arg Val Val Val Ala
 85           90           95
Cys Gly Ile Arg Gln Ala Arg Val Glu Val Glu Arg Phe Gly Gly Val
100           105           110
Leu Pro Glu Arg Ala His Gly Val Gly Gln Arg Asn Asn Arg Val Ala
115           120           125
Thr Asp Arg Leu Thr Asp Arg Met Pro Ile Asp Arg Gly Leu Gly Arg
130           135           140
Glu Pro Arg Ser Val Gly Gly Gln Ile Asp Arg Glu Arg Asp Gln Pro
145           150           155           160
Gln Arg Ile Pro Ala Gly Lys His Val Thr Pro His Cys Ser Gln Pro
165           170           175
Arg Ser Leu His Leu Val
180

```

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

```

Asn Asp Arg Leu Ile Ser Met Arg Asp Gly Gly Ile Val Ala Leu Pro
 1           5           10           15
Gln Leu Thr Asp Glu Gln Arg Ala Ala Ala Leu Glu Lys Ala Ala Ala
 20           25           30
Ala Arg Arg Ala Arg Ala Glu Leu Lys Asp Arg Leu Lys Arg Gly Gly
 35           40           45
Thr Asn Leu Thr Gln Val Leu Lys Asp Ala Glu Ser Asp Glu Val Leu
 50           55           60

```

218

Gly Lys Met Lys Val Ser Ala Leu Leu Glu Ala Leu Pro Lys Val Gly
 65 70 75 80
 Lys Val Lys Ala Gln Glu Ile Met Thr Glu Leu Glu Ile Ala Pro His
 85 90 95
 Pro Ala Ala Phe Val Ala Ser Val Thr Val Ser Ala Arg Pro Cys Trp
 100 105 110
 Lys Ser Ser Ala Pro Pro Asn Pro Ala Gly Arg Arg Cys Gly Pro Glu
 115 120 125
 Gly Leu Trp Trp Ala Tyr Pro Arg Ile Arg Gly Arg Ser Gly Leu Thr
 130 135 140
 Gly Pro Ala His Asn Ser Gly Arg Thr Pro Arg Trp Gly Gly Thr Arg
 145 150 155 160

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

Asp Trp His Arg Gln Pro Pro His Arg Gly Arg Ala Asp Gln His Leu
 1 5 10 15
 Gly Leu Asp Ala Arg Leu Cys Ala Ala Cys Asn Val Leu Leu Val
 20 25 30
 Asp Gly Val Gln His Arg Pro Gln Arg His Gly Pro Gly Pro Arg Phe
 35 40 45
 Gly Phe Pro Arg Val Val Val Ala Cys Gly Ile Arg Gln Ala Arg Val
 50 55 60
 Glu Val Gln Arg Phe Gly Gly Val Val Pro Glu Arg Ala His Gly Val
 65 70 75 80
 Gly Gln Arg Asn Asn Arg Val Ala Thr Asp Arg Leu Thr Asp Arg Met
 85 90 95
 Pro Ile Asp Arg Gly Leu Gly Arg Glu Pro Arg Ser Val Gly Gly Gln
 100 105 110
 Ile Asp Arg Glu Arg Asp Gln Pro Gln Arg Ile Pro Ala Gly Lys His
 115 120 125
 Val Thr Pro His Cys Pro Gln Pro Arg Ser Leu His Leu Val Leu Thr
 130 135 140
 Ser Arg Arg His Val Glu Arg Gln Arg His Arg Ala Glu Glu Gln His
 145 150 155 160
 Glu Val His Ala Gly Pro Leu Gly Gly Ala Ser Gln Ser Gln Ala Ala
 165 170 175
 Pro Arg

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
 (B) TYPE: nucleic acid